



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 123592

TO: Gerald G Leffers

Location: REM/2A69/2C70

Art Unit: 1636

Thursday, June 03, 2004

Case Serial Number: 09/769699

From: Alex Waclawiw

Location: Biotech-Chem Library

Rem 1A71

Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes

STIC-Biotech/ChemLib

123392

0865

From: Leffers, Gerald
Sent: Wednesday, June 02, 2004 2:59 PM
To: STIC-Biotech/ChemLib; Yucel, Irem
Subject: RE: 09/769,699

Can anyone give me a status update for this search? This is an After-Final case that has a fairly tight deadline on it. It would be very useful to be able to allow the claims if they are in fact free of any of the more recently issued patents and/or pending applications. Thank you for your help. Gerry Leffers

Gerald G. Leffers Jr., PhD
Primary Examiner, Art Unit 1636
Remsen Building, Room 02A69
(571) 272-0772

-----Original Message-----

From: Fredman, Jeffrey
Sent: Thursday, May 20, 2004 9:39 AM
To: STIC-Biotech/ChemLib
Cc: Leffers, Gerald
Subject: FW: 09/769,699

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Leffers, Gerald
Sent: Thursday, May 20, 2004 8:01 AM
To: Fredman, Jeffrey
Subject: 09/769,699

Hi Jeff, please approve a RUSH updated search of issued and pending files for SEQ ID NO: 2 of this application (~ 1,200 amino acid residues). This is an After-Final that may well be allowable. As always, thank you for your help.
Gerry

Gerald G. Leffers Jr., PhD
Primary Examiner, Art Unit 1636
Remsen Building, Room 02A69
(571) 272-0772

RECEIVED
JUN -2 2004
(STIC)

Point of Contact:
Alexandra Waclawiw
Technical Info. Specialist
~~GMT 6A02 Tel: 308-4491~~

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 6-3-04
Date Completed: 6-3-04
Searcher Prep/Review: 7
Clerical: _____
Online time: 7

TYPE OF SEARCH:
NA Sequences: 8
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): computer

OM protein - protein search, using SW model

Run on: June 3, 2004, 07:04:28 ; Search time 23 Seconds

(without alignments)

2700.263 Million cell updates/sec

Title: US-09-769-699-2

Perfect score: 6294

Sequence: 1 MENTOKTIVPTGPPGYYA.....DEFLDSGIPKHNNTMEM 1203

Scoring table: BLOSUM62

Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued_Patents_AA:*

1: /cn2_6_ptodata/2/iaa/5A_COMBO.pep:*

2: /cn2_6_ptodata/2/iaa/5B_COMBO.pep:*

3: /cn2_6_ptodata/2/iaa/6A_COMBO.pep:*

4: /cn2_6_ptodata/2/iaa/6B_COMBO.pep:*

5: /cn2_6_ptodata/2/iaa/PCITS_COMBO.pep:*

6: /cn2_6_ptodata/2/iaa/bactfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID
-	-	-	-	-	-

Result No.	Score	Query	Match	Length	DB ID	Description
1	3054	48.5	1452	4	US-09-127-227-2	Sequence 2, Appli
2	183	2.9	35	2	US-09-332B-9	Sequence 9, Appli
3	183	2.9	35	3	US-09-33B-876-9	Sequence 9, Appli
4	131	2.1	757	3	US-09-413-814-84	Sequence 84, Appli
5	123	2.0	1074	4	US-09-071-035-358	Sequence 358, Appli
6	123	2.0	1074	4	US-09-071-035-394	Sequence 394, Appli
7	122	1.9	1096	4	US-09-134-000C-5764	Sequence 5764, Appli
8	118	1.9	370	4	US-09-252-991A-16913	Sequence 16913, Appli
9	117	1.9	855	4	US-09-489-039A-12661	Sequence 1681, Appli
10	111	1.8	4630	4	US-09-091-609-2	Sequence 2, Appli
11	111	1.8	5215	3	US-09-105-537-2	Sequence 2, Appli
12	110	1.7	790	4	US-09-543-681A-6059	Sequence 6059, Appli
13	106	1.7	3567	3	US-07-642-734C-4	Sequence 4, Appli
14	106	1.7	3567	3	US-08-439-009A-4	Sequence 4, Appli
15	106	1.7	774	1	US-07-731-157A-7	Sequence 7, Appli
16	106	1.7	774	2	US-08-541-780-7	Sequence 7, Appli
17	105	1.7	1095	4	US-09-107-532A-3855	Sequence 3855, Appli
18	105	1.7	774	1	US-08-633-760-46	Sequence 46, Appli
19	105	1.7	774	1	US-08-633-760-48	Sequence 48, Appli
20	104	1.7	635	4	US-08-931-608A-5	Sequence 5, Appli
21	104	1.7	635	4	US-09-851-847-5	Sequence 5, Appli
22	104	1.7	774	1	US-08-019-870-5	Sequence 5, Appli
23	104	1.7	1471	4	US-08-811-519-1	Sequence 1, Appli
24	103	1.6	774	1	US-08-019-870-3	Sequence 3, Appli
25	103	1.6	774	1	US-08-633-760-44	Sequence 44, Appli
26	103	1.6	3472	4	US-09-408-020-4	Sequence 4, Appli
27	102	1.6	729	1	US-08-070-165F-6	Sequence 6, Appli

28	102	1.6	729	2	US-08-885-418-6	Sequence 6, Appli
29	102	1.6	774	1	US-07-147-901A-3	Sequence 3, Appli
30	102	1.6	774	1	US-07-53-760-50	Sequence 50, Appli
31	101	1.6	773	1	US-08-019-870-1	Sequence 1, Appli
32	101	1.6	773	1	US-08-019-870-6	Sequence 6, Appli
33	101	1.6	774	1	US-08-019-870-8	Sequence 8, Appli
34	101	1.6	774	1	US-08-019-870-11	Sequence 11, Appli
35	101	1.6	774	1	US-08-633-760-11	Sequence 52, Appli
36	101	1.6	995	4	US-09-057-931A-1	Sequence 1, Appli
37	101	1.6	995	4	US-09-568-180-5	Sequence 48, Appli
38	101	1.6	1024	4	US-09-562-337-48	Sequence 20, Appli
39	101	1.6	1466	4	US-09-262-337-20	Sequence 20, Appli
40	101	1.6	7257	3	US-09-235-409-5	Sequence 5, Appli
41	101	1.6	7257	4	US-09-567-870-5	Sequence 5, Appli
42	101	1.6	7257	4	US-09-567-969-5	Sequence 5, Appli
43	101	1.6	7257	4	US-09-568-180-5	Sequence 5, Appli
44	101	1.6	7257	4	US-09-568-186-5	Sequence 5, Appli
45	101	1.6	7257	4	US-09-568-412-5	Sequence 5, Appli
46	101	1.6	7257	4	US-09-567-899-5	Sequence 5, Appli
47	100	1.6	1321	5	US-08-261-822A-3	Sequence 3, Appli
48	100	1.6	1321	5	PCT-US55-0744A-3	Sequence 3, Appli
49	100	1.6	2616	6	5206163-3	Patent No. 5206163
50	100	1.6	1381	4	US-09-08-701A-25	Sequence 25, Appli
51	99.5	1.6	600	4	US-09-252-991A-29817	Sequence 29817, A
52	99	1.6	915	4	US-09-151-500A-25	Sequence 25, Appli
53	98.5	1.6	910	4	US-09-134-000C-4288	Sequence 4288, Ap
54	98.5	1.6	910	4	US-09-036-987A-3	Sequence 3, Appli
55	98.5	1.6	2152	3	US-09-370-700-3	Sequence 3, Appli
56	98.5	1.6	2152	4	US-09-093-207-3	Sequence 3, Appli
57	98.5	1.6	2152	4	US-09-251-991A-24209	Sequence 24209, A
58	98	1.6	551	4	US-08-451-822A-13	Sequence 13, Appli
59	98	1.6	821	2	US-09-323-830-13	Sequence 13, Appli
60	98	1.6	821	4	US-09-252-991A-19282	Sequence 19282, A
61	97.5	1.5	660	4	US-08-411-510-8	Sequence 8, Appli
62	97.5	1.5	769	1	US-09-162-737-50	Sequence 7973, Ap
63	97.5	1.5	1024	4	US-09-489-039A-1973	Sequence 2, Appli
64	97.5	1.5	2680	4	US-08-173-508-2	Sequence 2, Appli
65	97	1.5	537	2	US-08-365-310-2	Sequence 2, Appli
66	97	1.5	537	3	US-08-951-742-2	Sequence 2, Appli
67	97	1.5	1469	4	US-09-262-537-58	Sequence 58, Appli
68	97	1.5	522	4	US-09-543-681A-7785	Sequence 7785, Ap
69	96.5	1.5	987	4	US-09-053-681A-7785	Sequence 7785, Ap
70	96.5	1.5	987	4	US-09-543-681A-7785	Sequence 7785, Ap
71	96	1.5	774	1	US-08-314-309A-21	Sequence 21, Appli
72	95.5	1.5	3170	3	US-08-642-734C-5	Sequence 5, Appli
73	95.5	1.5	3170	3	US-08-439-009A-5	Sequence 5, Appli
74	94.5	1.5	500	4	US-09-071-035-396	Sequence 396, Ap
75	94.5	1.5	817	4	US-09-189-039A-10407	Sequence 10407, A
76	94.5	1.5	1013	4	US-09-180-245-2	Sequence 2, Appli
77	94.5	1.5	6095	3	US-09-194-052-508	Sequence 5508, Ap
78	94	1.5	655	1	US-07-736-178C-2	Sequence 2, Appli
79	94	1.5	94	1.5	US-18-166-318-183	Sequence 2, Appli
80	94	1.5	2910	2	US-08-144-733-183	Sequence 183, Ap
81	94	1.5	2910	2	US-08-164-134-183	Sequence 183, Ap
82	94	1.5	2910	2	US-08-361-183	Sequence 183, Ap
83	94	1.5	2910	2	US-08-456-910-183	Sequence 183, Ap
84	94	1.5	2910	5	PCP-US90-06266-157	Sequence 2, Appli
85	94	1.5	2910	5	US-09-556-824-2	Sequence 2, Appli
86	94	1.5	3589	4	US-09-548-452A-153	Sequence 153, Ap
87	93.5	1.5	544	4	US-09-801-788-1	Sequence 1, Appli
88	93.5	1.5	3241	4	US-09-649-616-3	Sequence 3, Appli
89	93.5	1.5	1113	3	US-08-744-490-10	Sequence 10, Appli
90	93.5	1.5	1177	3	US-08-413-814-10	Sequence 12, Appli
91	93.5	1.5	1177	3	US-08-450-332-2	Sequence 10, Appli
92	93.5	1.5	3038	2	US-08-637-640-2	Sequence 12, Appli
93	93.5	1.5	3038	3	US-09-004-406C-2	Sequence 2, Appli
94	93	1.5	3241	4	US-09-801-788-1	Sequence 1, Appli
95	93	1.5	1113	3	US-09-649-616-3	Sequence 3, Appli
96	93	1.5	1177	3	US-08-744-490-10	Sequence 10, Appli
97	93	1.5	1177	3	US-08-450-332-2	Sequence 12, Appli
98	93	1.5	1177	3	US-08-922-505A-12	Sequence 12, Appli
99	93	1.5	1177	3	US-09-260-952A-10	Sequence 12, Appli
100	93	1.5	1177	3	US-09-250-952A-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
i Sequence 2, Application US/09127227
i General Information:
i Patent No. 639934
i Applicant: David M. Knipe
i Applicant: Elizabeth McNamee
i Title of Invention: Replication-Competent Virus Expressing A
i File Reference: HU98-05
i Current Application Number: US/09/127,227
i Current Filing Date: 1998-07-31
i Number of SEQ ID NOS: 6
i Software: FastSSQ for Windows Version 3.0
i SEQ ID NO: 2
i LENGTH: 1452
i TYPE: PRT
i ORGANISM: herpesvirus
US 09-127-227-2

Query Match 48.5%; Score 3054; DB 4; Length 1452;
Best Local Similarity 49.8%; Pred. No. 2.7e-304; Indels 48; Gaps 17;
Matches 609; Conservative 200; Mismatches 366; Length 1452;

Qy 1 MENTQKTT--VPTGPIGLVY--ACRVEDDLEIISFLAARSTDSDLALLPLMRNTE 55
Db 1 METKPKTATTIKVPGPGLVYVYARACPSRKL--LALLSARSADAYAVAPIVGVLT 58

Qy 56 KTFPTSSLAVVYSGARTGAGITIKLTLTHPPGCKHVLPSAAAPNLUTRACNA 115
Db 59 SGFEANAVAVVYGSRTGGLGTTAVSLKLTHPSHYSVSVVPHGRHLDPSTQAPNLTRLCR 118

Qy 116 ARERFGFSRCOGPPVVDGAETTGAEICTRIGLEPENTIYLVLTALFKEARVMCNVFLHY 175
Db 119 ARRHRGFSDYTPRPGDQLKHEETGEALCERGLDPRALLYLVTEGKFREAVCINNTFLHL 178

Qy 176 GGDLTHINNGDVTRIPFLPVQLMPDFVNLPDPFNTTHRSIGEGFYVPTPPFTNGLCH 235
Db 179 GSdKvTIGGASVHRIPVPLQLMFDPSRVIAEPNANHRSIGENFTPLPFENRPLNR 238

Qy 236 LIHDCVIAPMAYALVRYNTNTAVARGAHAHLAFDENHEGAVLFPDITYTYFQSSSSGTITAR 295
Db 239 LLFEATVGPAAVALCRNNDVAVARAAAHLADEFEGALAPDTFTABEASQG--KTPR 296

Qy 296 GARRNDVNSTSKPSPGGGFERLASMIAUTALHAEVINTGTYEETPDIKEWPMETGM 355
Db 297 GGR-----DGSGKGPGAGFEEQRLASMAQDAALESTISMAVEBPPDTSAMPCLCBOQ 351

Qy 356 EGTLPRLNAGSYTAEVGIVAMVFSPINSALYDEVESGMTEAKDGGPGPSFNRFYCF 415
Db 352 DTAARANANVGRAYLAAAGLNGAMFESTNSALHLTEVDAGPADEKDHSK-PSYRFFLY 410

Qy 416 AGPHLAAAPQTDRDGHVL-----SSQSTGSNTTEFSDYALICGFAPILLFL 468
Db 411 FGTHVAANPQDREGHTVPGFEGRPAPLVGSTQ-BFAGEHLMCGFSPALLAKMFL 469

Qy 469 ERCDAGAGFTGGHG-DALKYTGTCDFSEIPCSLCEKHTRPGCAHTTVHRQRMPREGQT 527
Db 470 ERDGGYTIVGRDEMDFYRVAQDSNQDPCNLCFTDRACTVHTILMRBRRHKPASIA 529

Qy 528 ROPIGVFGTMNSQYSDCDPENYAPYLIRKPGDQEAKMDTYRATERLFLDIEQ 587
Db 530 RGAIGVFTGTMNSQYSDCDPENYAPYLIRKPGDQEAKMDTYRATERLFLDIEQ 588

Qy 588 ERLLDRGAPCSSEGLSSVIVDHPTRRIIDLTARAEQTTOFMRKVLYTERDYKIREGJS 647
Db 589 LQYDQAVPTANGRLTITNREALHTVNNVRQVDRVEQMLNVLGEGRNFXRDGJG 648

Qy 648 EATHSMALTFDPYSGAFCPITNFVLRKRTHLAVVODLALSQCHCVYGOOYEGRNFRNQFQ 707
Db 649 EAHNAMSLLTDPIAGCPCLQOLIGRSNIAVYDODLALSQCHGVAGQSVEGRNFRNQFQ 708

Qy 708 PYLRRFVDFLFGCPTISTRITYTTLSEG-PVSAPNPTLGQDAPAGRIFPDGLARVSVEI 766
Db 709 PYLRRFVMDENNGPLSAKLTVALSEGAICAPSLSLAGTQTAPESSFBGDVARVTLGPP 768

Qy 767 RDIRKGNRIVYFSGNTNLSPAAARLVLGLASAYORQEKVDMFLGALGELLKQPHGLLPP 826
Db 769 KELRVTSRVLFGAGSANASAAKARVASHQSAYQDKEVLDLQGFLKQPHAIIFP 828

Qy 827 RGMPNPKSPNPQWFMILLORNONPADKLTHEETTIAVAKRKFTEYYAAINPINLPTCI 886
Db 829 NGKPPSNQPNPQWFMILLORNONPADKLTHEETTIAVAKRKFTEYYAAINPINLPTCI 888

Qy 887 GELAQFYMANLILKCYCDHSQYLINTLTSIITGARRPDPSSVLWIKRDVTSAAIDTOA 946
Db 889 SELAMNTMANOLRYCDHSTYPPINTLTLAGSRPSPVQAAAAM--SAQGGAGLEAGA 945

Qy 947 KALLEKTENPLBLWTAFTSTHLYRAAMNRPMTYLVGSIISKYHAGNRFQGNGWSG 1006
Db 946 RALMDAVDAHGAWSMFAASCNLLPFPVMAARPMTVGLSISKYGMAGNDRFQGNGWSG 1005

Qy 1007 LNGGKRNVCPLTEDRTRFLIACPRGFCICPTVGBSCNREBTLSQDVQRTGIVTSGAMVQ 1066
Db 1006 LMGGKRNACPLIFDRTRFLIACPRGFCVACNIGGAHESSLQLRGITISEGRANA 1065

Qy 1067 LAIYATVTRAYCARGAOMAFDWLSITDDEFLARDLBEHQIOLIOTLETWTVEGAL-- 1123
Db 1066 SSVFVATVKSLGPRTQLOQDITDWLALDEYLSMELTALARLGNGEWSTDALLEVA 1125

Qy 1124 -BAVKLDEKITAOGDFTPINLAFND--SECPBSHATTSVNINISSNSNISGSTVPGKLRP 1180
Db 1126 HRAEALVSQLNAGE-----VFNQDFGCE----DDNATPPFGCPGAPGPAFAGRKRA 1173

Qy 1181 PBDDELDSLSPKIRKGNTNM 1203
Db 1174 FHGDDPFG-EGFPDKQDITDM 1195

RESULT 2
US-08-007-332B-9
i Sequence 9, Application US/08807332B
i General Information:
i Patent No. 5959074
i Computer Readable Form:
i Medium Type: Floppy disk
i Computer: IBM PC Compatible
i Operating System: PC-DOS/MS-DOS
i Software: PatentIn Release #1.0, Version #1.30
i Current Application Data:
i Application Number: US/08/807,332B
i Filing Date: 28-FEB-1997
i Classification: 435
i Attorney/Agent Information:
i Name: Kovariik, Joseph E.
i Registration Number: 33,005
i Reference/Docket Number: 2879-39
i Telecommunication Information:

TELEPHONE: 303/863-9700
 TELEFAX: 303/863-0223
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-807-332B-9

Query Match 2.9%; Score 183; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.6e-11;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 545 DPLGNYAPYLRLRKPGDQTEAAKATMDDTYRATLE 579
 Db 1 DPLGNYAPYLRLRKPGDQTEAAKATMDDTYRATLE 35

RESULT 3
 US-09-338-876-9
 Sequence 9, Application US/09338876
 Patent No. 6187584
 GENERAL INFORMATION:
 APPLICANT: Dreyfus, David H.
 APPLICANT: Gefand, Ervin W.
 TITLE OF INVENTION: PRODUCTS AND PROCESSES FOR RECOMBINATION OF
 TITLE OF INVENTION: GENE RECOMBINATION OF
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sheridan Ross
 STREET: 1700 Lincoln St., Suite 3500
 CITY: Denver
 STATE: CO
 COUNTRY: U.S.A.
 ZIP: 80203

COMPUTER READABLE FORM:
 COMPUTER: IBM PC Compatible
 COMPUTER: PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATE:
 APPLICATION NUMBER: US/09/338,876
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/807,332
 FILING DATE: 28-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Kovariik, Joseph E.
 REGISTRATION NUMBER: 33,005
 REFERENCE/DOCKET NUMBER: 2879-39
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303/863-9700
 TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-338-876-9

Query Match 2.9%; Score 183; DB 3; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.6e-11;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 545 DPLGNYAPYLRLRKPGDQTEAAKATMDDTYRATLE 579
 Db 1 DPLGNYAPYLRLRKPGDQTEAAKATMDDTYRATLE 35

RESULT 4
 US-09-413-814-84
 Sequence 84, Application US/09413814
 Patent No. 6225064
 GENERAL INFORMATION:
 APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 APPLICANT: Bristol-Myers Squibb, Co.
 APPLICANT: Bleyer, Stefan
 APPLICANT: Brandt, Helmut
 APPLICANT: Dougherty, Brian A
 APPLICANT: Lino, Paul M
 APPLICANT: Goldberg, Steven L
 APPLICANT: Hofle, Gerhard
 APPLICANT: Mueller, Joachim
 APPLICANT: Reichenbach, Hans
 TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
 TITLE OF INVENTION: heteropolyketide compounds
 FILE REFERENCE: PCT/US 99/23535
 CURRENT APPLICATION NUMBER: US/09/413-814
 CURRENT FILING DATE: 1999-10-07
 EARLIER APPLICATION NUMBER: DE 198 46 493.2
 EARLIER FILING DATE: 1998-10-09
 NUMBER OF SEQ ID NOS.: 107
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 84

Query Match 2.1%; Score 131; DB 3; Length 757;
 Best Local Similarity 21.1%; Pred. No. 0.0012;
 Matches 146; Conservative 84; Mismatches 251; Indels 212; Gaps 37;

Qy 54 VPKFTPSLAVVSGART --- TGLAGGAGITKLTKTSHFYPSPVVFHIGKHYLPSSAPN 109
 Db 129 LERTLPVASYIVADAREAAALTSSAVGIVAS----- LPASAA-- 167

Qy 110 TRACNAARERFGSRCGPVPGDAEVITGAETCTRIGLEPENTILLYVVTALFKEA 169

Db 168 ----- ALQRQRWTATDQPS -RPIIEGPGA ----- AIRPESV----- 198

Qy 170 NVFLHY --- GGLDIYHINHGDVIRIPLFPVQLFMDVNRLVPDPFNTHRSIGEFGVY 224

Db 199 -AFQYTSSTGPKGMLTHNL --- LENSRLIAHGFDLTSPDVY----- GVIV 244

Qy 225 PTFFYNTGLC----- HLTHDCVIAPMAYALR --- VRNVTAV -- ARGAAHIAFD- 267

Db 245 LPPYHDMLGLIGIQLQALYRRIRVALMSPSLQRPWRLAVSALGASVSGGPNFAYDLC 304

Qy 268 --- ENHESAVLPDITYTYFQSSSSTTARGARDNVTNSTSKPEPGGPERLASSIVA 323

Db 305 VRKSEEERAAID----- LSWEVFTGAPVRAIDLFRAPVSRVRE -AFYP 355

Qy 324 ADTALHAEVIENTGIVETPTDIKEWMFIGMEGTPLRNALGSYTPARVAVGIGMF-- 381

Db 356 CYGLAEATLIVSGAREAPV----- LARLAPEEVLRVAVASAE -GARFVG 403

Qy 382 --- SPNSALVLTTEVEDSGMTAEKDGPGPSENRYQFAGPHLA -ANPQTDRDGHV 432

Db 404 SGRALDPPA -- VAIVDPAG -- NEIHPG-EIGEINW-VSSPSVAVGYSERPE----- 447

Qy 433 LSSQSTGSNTERSVUDLALIGFGAFLLLFLIERCDAGAFCGHGDALKYVTGT- 490

Db 448 ----- ETETATGATLAGSAAPR ----- YLTGDLGFLRGCB --- LFVYGRSK 486

Qy 491 ----- FSEIIPSLCETH -TRPVC -AHITVHR.LQRM ----- PRFGOATRQ 529

Db 487 DLIILRGHNFQDIECTVSESSHRAVPGCSAAFSYHEGERLVAVCEVDPRVAAADPRE 546

Qy 530 PIGVFGTMNSQYSDDPLGNTAPYLRLRKPGDQTEAAKATMDDTYRATLERLFTDLEQER 589

RESULT 5

US-09-071-03-358
 Sequence 358, Application US/09071035
 Patent No. 6448043
 GENERAL INFORMATION:
 APPLICANT: Gil H. Choi
 TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 NUMBER OF SEQUENCES: 496
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,035
 FILING DATE:
 CLASSIFICATION:
 APPLICATION NUMBER:
 PILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: A. Anders Brookes
 REFERENCE NUMBER: 36 373
 REFERENCE/DOCKET NUMBER: PB169P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEX/FAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 358:
 CHARACTERISTICS:
 LENGTH: 1074 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-09-071-035-358

Query Match Score 2.08; Length 1074;
 Best Local Similarity 18.3%; Pred. No. 0.016;
 Matches 206; Conserved 150; Mismatches 415; Indels 352; Gaps 52;

Query 250 RVRNTAVARGAHLAPDENHGAVALPPDITYTFOSSSGTTARGARRNDVNISTSKS 309
 Db 67 RTTSLYAYNGAKQTVPC-TERGVSIPTEVTHGY-----OKPL 104

Query 310 PSSGFERLASM--ADDTALHAEVFTNTGIVEE-----TPTDIKEWPMF 353
 Db 105 PSMSDKAKLVSVLWERAKTDIDTNMVAQKHWEEVNGYKLHSIKRLGGASVDIK-----158

Query 354 GMETGLPPMLNAGSYTAR-----VAGVIG-AMVFSNPNALYLTVEPSGMTEAKDGGP 405
 Db 159 SIEGKINK--AEEYQKKEPSFNNTVTKTILQGSTLNLSEFDKVQVQNTA-----211

Query 406 GPSENRFYQFAGPHLAAPQTDRGHVLSSOSTGSNTTEFSDVTLALICFGAPLLARL 465

Db 547 IVAREATAEHQ----IYAHAVALIAGPALPKTSICKRVERCRERAFL-----DALGR 598
 Qy 590 ----ILDRGAPCSSSGLSSVIVDHPTRFLDLRLEQTTOQFMKVLFTRDJKI 642
 Db 599 HVAFAPELDDASPPDD---APPETEPEPSGRSLDLARS----TLLARALRDLAQIDDL 651
 Qy 643 ---REGL-SEATISMALTFDPVSYGAFCPITNPL 671
 Db 652 PISRFGLDSLAAYELQHAFQVRTGRTGRATPLTSL 684

Db 359 SMTSKMNROCKQQILKETG-VETGDLWMDNYSLAGNTFAIREDSAGBHVOPITTDQKG 417
 Db 622 RIEQTTOQFMKVLFTRDJKIREGLSEATHSMALTPD-----YSGAFCPITNFLVJRT 675
 Db 418 RAE--TPKELANALEHTGTYVTE--TKSSNGFYNTFKPTKVELKYANQTVALVTSNPKGQ 473
 Qy 676 HIAVVDLAL-----SOCHCVFYQGV-----EGANFRNQFQPVURRFYVDL 717
 Db 474 NOBITGETTLTKEKDGTGNEQSQKAFTGKAETYLIFTAKDQAVKWSAEFK-----TEL 526
 Db 527 VKGTKASDETTILALDEKNOVAVHLAINEFWOTKABEGTYLDETKYPVSIKKVDNN 586
 Qy 765 ---VIRDIRVKNRYV-----FSGNCNTNLSEAA-----RARLYGLASAYQROEKR 805
 Db 587 KNAVIRDVTAKEQ/TIRGFDFKFKPGASDGTGFLSFKVSPLSGTXET-TGAEDKA 646
 Qy 806 VDMLHGALGP-----LLKOFHGLLPRGM-----PENSKS-----PNP 838
 Db 647 TTACNQQLQGLPFGYGYKFENLPYGDYLLE/EA--PEGQKITLEIRSTPKENKDVAKS 703
 Qy 839 QWFWTLLQRNQ-----MPADKLTHETITIAAVKRFTEEYAAINSTNL-----PTCTGE 888
 Db 704 BYVFTITEEGOKOPTIMVTPYBKLNNE-----FSVSLNRLMLYDLPERKEDSLS 754
 Qy 889 LAQFYMANLILKYCDHSQVJINTLTSITGARRBDPSSVLPKIRD-----VTSAADEBTQ 945
 Db 755 LATWKGNKCLNTLDFTE-LVDKL-----RYNLHEIKEDWVVAQADBEA- 799
 Qy 946 AKALLEKTNELPELTATFATST-----HYRAAMNQRPVYVULGJSISKHGA 992
 Db 800 TKAQQKDEKAVPKVVAETTALANKETGTWKILHKLTAEQ-----VLDKSVLNYV 853
 Qy 993 AGNNRQFAGNWSGNGGGRNVNCVPDFTDRTRFLIACPRGGFTOPVTPGSSGNRETLLSD 1052
 Db 854 YENKV/FEAGNE-----PVA-----KDASLNN 875
 Qy 1053 QVRGITVSGGAMVQIAIAYVVRAGAR-----AOMNAFDWLSLTDDEFLARDL-- 1102
 Db 876 QAQ-----TVNCTIERHVISQTKAHLLEDGSQFTFHGDVMMDDVSVTHVLD 923
 Qy 1103 --BEHDQIQTLETPTVTEGALKVILDE-----KTTAGD-----GETPINLAFNFD 1149
 Db 924 GSKEAEFTIYLALLDGTINKEIWGKEHEVNDKEFKTKVLAERDKYFEGTKFPE- 992
 Qy 1150 SCEPSPHDTTSRV-----LNSGSNNSGTSVPLKRPBEPDE 1185
 Db 983 -TEINYERDGVNGKHINEDLKKSQTLPKEVPTIPSPKQE 1024

RESULT 6

US-09-071-035-394
 Sequence 394, Application US/09071035
 Parent No. 6448043
 GENERAL INFORMATION:
 APPLICANT: Gil H. Choi
 TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 NUMBER OF SEQUENCES: 496
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION NUMBER: US/09/071-035
 APPLICATION NUMBER: US/09/071-035
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: A. Anders Brookes
 REGISTRATION NUMBER: 36-373
 REFERENCE/DOCKET NUMBER: PB369P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 SEQUENCE CHARACTERISTICS:
 LENGTH: 104 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-071-035-394

Query Match 2.0%; Score 123; DB 4; Length 1074;
 Best Local Similarity 18.3%; Pred. No. 0.016;
 Matches 206; Conservative 150; Mismatches 415; Indels 352; Gaps 52;

Qy 250 RVRNVTAVARGAAHLADEFNENHEGAVLPPDITYTYFOSSSSGTTARGARRNDVNSTS KPS 309
 Qy 67 RTTSVYAEINGAKQTVFC-TEPGVSIPTETGY-----QRNP 104

Qy 310 PSGGFERRASIM-AADTAHALVIENTGIVEE-----TPTDIKEWPMFI 353
 Db 105 PSMDSKAKVSVSLWEKAQTDIDTNNAVAQCMWVNGYKLHSIKRGLGASVDIK-----158

Qy 354 GMGETLPLRNALGSYTA-----VAGTG-ANVFSNPSALVLTEDSGMTBAKOGGP 405
 Db 159 SIEGKINK-AIEEYOKKPSFHNTTVKTIGOSTTLIDKNELNISEFKVQNTA-----211

Qy 406 GPSFNRFYOFAGPHIAANPOTDRDGHVLSSQSTGSSNTFSVYDYLICFGAPILLRL 465
 Db 212 ---NIDVYRIGNQLVLT-----NSNSKSGTTLIKKIDKESEGVDTKGTGP-VAYKK 251

Qy 466 FYLERCDAGAFTGGHGDALKYVTGSTFDSIIPCSCEKTRTRPVCAHTTVHLRQRMPREGQ 525
 Db 252 AGLQTVWAGALDKPPTYAKIKINVERTKGS-LKIKIDKESEGVDTKGTGP-DGK 304

Qy 526 A-----TROPIGVFGTMNSQYSPCDPLOGNYA-----PYLLRKPGDQEAAKATM 570
 Db 305 ALPSKDVTDKDGI-----SILDGIPHGTKVTEKSYPDPWMIDTPMAAIIKAGETI 358

Qy 571 QDTYTRATLBFIDLEQERLDRGAPCSSEGSL-----SVIVDHP-----FRBLDILRA 621
 Db 359 SMTSKOMRQGQNLKETKG-VETGTDLNNDYSLAGNTPAIRDSPANBIVQETTDEKG 417

Qy 622 RIEQTTOFMKVLYETRDYKIREG-----SEATHSMALTFDP-----YSGACFPITNFLYVKT 675
 Db 418 RAE-TPKELANALLGTYVTE-TKSNGFVNTFKPKPVKELYKANOTVALTSNTYKG 473

Qy 676 HLAVQDALL-----SQCICVYFGSQV-----EGRNFRNQFQPVLRRRFYD 717
 Db 474 NQEITGETLTKEDXDTGNESQKAETFLTAKINGQAVKWSREAK-----TEL 526

Qy 718 FNGGGFISTRSTRSTVLSSE-GPVSAPNTLQG-----DAPAGRTFOODLARVSV-----764
 Db 527 VRGTAKADETVTLALDEKNCVAKHAINEFWQEETKAPEGYLTDDTKTPSISKKVDNNE 586

Qy 765 ---VDIRIVKNRYV-----PGNCNTNLSEAM-----RARLUGLASAYQOEKR 805

Db 587 KNVITTDVTAKEQVTRGFDFKPKLGSDADTAETFDNLSFKVSLEGTXEITGAEKA 646
 Qy 806 VDMLHAGLF-----LIKQFHGLLPFGM-----PNNSKS-----PNP 838

Db 647 TTACNEQLGFDSYKGPKENPGLYDYLJEEIA-----PEGFQKITPLEIRSTFKENKDQYAKS 703

Qy 839 QWFWTLLQRNO-----MPADKLTHEITIAVTRFTEYAAVTRF-----FSVSLNRMLYDLPKEKEDSLS 754

Db 704 EVUTTIEEGQXQPIMVNTVPEKLNN-----VLRKSVIYNVY 853

Qy 889 LAQFYMANLILKYCDSQYINTLTSTITGARRPRDPSSVHLWIRD-----VTSAAIDIETQ 945

Db 755 LATWDENKCNLTDFTB-LVDKL-----RYNHEIKDWYVAQALIVEA-799

Qy 946 AKALLEKTENLPELWTAFTST-----HYVRAMNORMPMVVLGJISISKYHGA 992

Db 800 TKAQOEKDEKARPVVIAETTATLANEKGTGTWKILKLTAEQ-----VLRKSVIYNVY 853

Qy 993 AGNNRVIQAGNWGLNGGRNVCPFTGPRGGFICPVTGSSGNRETFLSD 1052

Db 854 YENKVAPAGNE-----PVA-----KDSLNN 875

Qy 1053 QVRGIVTSGGANVQLLAIYATVRAVBAR-----AQEMAFFDMWLSLTDBBEFLARDL--1102

Db 876 QQQ-----TVCNTERTVITQTKAHLEDQSQTTHGVDMDFTDVLD 923

Qy 1103 --BELHDPQIQLTETPTVGEALEAKTILDE-----KUTAGD-----GETPTNLAFNFD 1149

Db 924 GSREAAFTTIALLPDTNKRKTIWKSKEIEHVNDKEFTKTVLAEKDTGKTPGTRKFTF-982

Qy 1150 SSEPSPHTTSNV-----INISGNSISGTVPLKRPEDDE

Db 983 -TEINTVKDQGNTNGKHINEDLKSKQSLTPKRVPTIPSTPXEPE 1024

RESULT 7
 US-09-134-000C-5764
 Sequence 5764, Application US/0913400C
 Patent No. 6617156
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FACALIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 PRIORITY APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: Patent in version 3.1
 SEQ ID NO: 5764
 TYPE: PCT
 ORGANISM: Enterococcus faecalis
 US-09-134-000C-5764

Query Match 1.9%; Score 122; DB 4; Length 1096;
 Best Local Similarity 18.5%; Pred. No. 0.02;
 Matches 208; Conservative 149; Mismatches 410; Index 360; Gaps 53;

Qy 250 RVRNVTAVARGAAHLADEFNENHEGAVLPPDITYTYFOSSSSGTTARGARRNDVNSTS KPS 309

Db 89 RTTSVYAEINGAKQTVFC-TEPGVSIPTETGY-----QRNP 104

Qy 310 PSGGFERRASIM-AADTAHALVIENTGIVEE-----TPTDIKEWPMFI 353

Db 105 PSMDSKAKVSVSLWEKAQTDIDTNNAVAQCMWVNGYKLHSIKRGLGASVDIK-----158

Qy 354 GMGETLPLRNALGSYTA-----VAGTG-ANVFSNPSALVLTEDSGMTBAKOGGP 405

Db 159 SIEGKINK-AIEEYOKKPSFHNTTVKTIGOSTTLIDKNELNISEFKVQNTA-----211

Qy 406 GPSFNRFYOFAGPHIAANPOTDRDGHVLSSQSTGSSNTFSVYDYLICFGAPILLRL 465

Db 212 ---NIDVYRIGNQLVLT-----NSNSKSGTTLIKKIDKESEGVDTKGTGP-VAYKK 251

Qy 466 FYLERCDAGAFTGGHGDALKYVTGSTFDSIIPCSCEKTRTRPVCAHTTVHLRQRMPREGQ 525

Db 252 AGLQTVWAGALDKPPTYAKIKINVERTKGS-LKIKIDKESEGVDTKGTGP-DGK 304

Qy 526 A-----TROPIGVFGTMNSQYSPCDPLOGNYA-----PYLLRKPGDQEAAKATM 570

Db 305 ALPSKDVTDKDGI-----SILDGIPHGTKVTEKSYPDPWMIDTPMAAIIKAGETI 358

Qy 571 QDTYTRATLBFIDLEQERLDRGAPCSSEGSL-----SVIVDHP-----FRBLDILRA 621

Db 359 SMTSKOMRQGQNLKETKG-VETGTDLNNDYSLAGNTPAIRDSPANBIVQETTDEKG 417

Qy 622 RIEQTTOFMKVLYETRDYKIREG-----SEATHSMALTFDP-----YSGACFPITNFLYVKT 675

Db 418 RAE-TPKELANALLGTYVTE-TKSNGFVNTFKPKPVKELYKANOTVALTSNTYKG 473

Qy 676 HLAVQDALL-----SQCICVYFGSQV-----EGRNFRNQFQPVLRRRFYD 717

Db 474 NQEITGETLTKEDXDTGNESQKAETFLTAKINGQAVKWSREAK-----TEL 526

Qy 718 FNGGGFISTRSTRSTVLSSE-GPVSAPNTLQG-----DAPAGRTFOODLARVSV-----764

Db 527 VRGTAKADETVTLALDEKNCVAKHAINEFWQEETKAPEGYLTDDTKTPSISKKVDNNE 586

Qy 765 ---VDIRIVKNRYV-----PGNCNTNLSEAM-----RARLUGLASAYQOEKR 805

Db 587 KNVITTDVTAKEQVTRGFDFKPKLGSDADTAETFDNLSFKVSLEGTXEITGAEKA 646

Qy 806 VDMLHAGLF-----LIKQFHGLLPFGM-----PNNSKS-----PNP 838

Db 647 TTACNEQLGFDSYKGPKENPGLYDYLJEEIA-----PEGFQKITPLEIRSTFKENKDQYAKS 703

Qy 839 QWFWTLLQRNO-----MPADKLTHEITIAVTRFTEYAAVTRF-----FSVSLNRMLYDLPKEKEDSLS 754

Db 704 EVUTTIEEGQXQPIMVNTVPEKLNN-----VLRKSVIYNVY 853

Qy 889 LAQFYMANLILKYCDSQYINTLTSTITGARRPRDPSSVHLWIRD-----VTSAAIDIETQ 945

Db 755 LATWDENKCNLTDFTB-LVDKL-----RYNHEIKDWYVAQALIVEA-799

Qy 946 AKALLEKTENLPELWTAFTST-----HYVRAMNORMPMVVLGJISISKYHGA 992

Db 800 TKAQOEKDEKARPVVIAETTATLANEKGTGTWKILKLTAEQ-----VLRKSVIYNVY 853

Qy 993 AGNNRVIQAGNWGLNGGRNVCPFTGPRGGFICPVTGSSGNRETFLSD 1052

Db 854 YENKVAPAGNE-----PVA-----KDSLNN 875

Qy 1053 QVRGIVTSGGANVQLLAIYATVRAVBAR-----AQEMAFFDMWLSLTDBBEFLARDL--1102

Db 876 QQQ-----TVCNTERTVITQTKAHLEDQSQTTHGVDMDFTDVLD 923

Qy 1103 --BELHDPQIQLTETPTVGEALEAKTILDE-----KUTAGD-----GETPTNLAFNFD 1149

Db 924 GSREAAFTTIALLPDTNKRKTIWKSKEIEHVNDKEFTKTVLAEKDTGKTPGTRKFTF-982

Qy 1150 SSEPSPHTTSNV-----INISGNSISGTVPLKRPEDDE

Db 983 -TEINTVKDQGNTNGKHINEDLKSKQSLTPKRVPTIPSTPXEPE 1024

RESULT 7
 US-09-134-000C-5764
 Sequence 5764, Application US/0913400C
 Patent No. 6617156
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FACALIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 PRIORITY APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: Patent in version 3.1
 SEQ ID NO: 5764
 TYPE: PCT
 ORGANISM: Enterococcus faecalis
 US-09-134-000C-5764

Query Match 1.9%; Score 122; DB 4; Length 1096;
 Best Local Similarity 18.5%; Pred. No. 0.02;
 Matches 208; Conservative 149; Mismatches 410; Index 360; Gaps 53;

Qy 250 RVRNVTAVARGAAHLADEFNENHEGAVLPPDITYTYFOSSSSGTTARGARRNDVNSTS KPS 309

Db 89 RTTSVYAEINGAKQTVFC-TEPGVSIPTETGY-----QRNP 104

Qy 310 PSGGFERRASIM-AADTAHALVIENTGIVEE-----TPTDIKEWPMFI 353

Db 105 PSMDSKAKVSVSLWEKAQTDIDTNNAVAQCMWVNGYKLHSIKRGLGASVDIK-----158

Qy 354 GMGETLPLRNALGSYTA-----VAGTG-ANVFSNPSALVLTEDSGMTBAKOGGP 405

Db 159 SIEGKINK-AIEEYOKKPSFHNTTVKTIGOSTTLIDKNELNISEFKVQNTA-----211

Qy 406 GPSFNRFYOFAGPHIAANPOTDRDGHVLSSQSTGSSNTFSVYDYLICFGAPILLRL 465

Db 212 ---NIDVYRIGNQLVLT-----NSNSKSGTTLIKKIDKESEGVDTKGTGP-VAYKK 251

Qy 466 FYLERCDAGAFTGGHGDALKYVTGSTFDSIIPCSCEKTRTRPVCAHTTVHLRQRMPREGQ 525

Db 252 AGLQTVWAGALDKPPTYAKIKINVERTKGS-LKIKIDKESEGVDTKGTGP-DGK 304

Qy 526 A-----TROPIGVFGTMNSQYSPCDPLOGNYA-----PYLLRKPGDQEAAKATM 570

Db 305 ALPSKDVTDKDGI-----SILDGIPHGTKVTEKSYPDPWMIDTPMAAIIKAGETI 358

Qy 571 QDTYTRATLBFIDLEQERLDRGAPCSSEGSL-----SVIVDHP-----FRBLDILRA 621

Db 359 SMTSKOMRQGQNLKETKG-VETGTDLNNDYSLAGNTPAIRDSPANBIVQETTDEKG 417

Qy 622 RIEQTTOFMKVLYETRDYKIREG-----SEATHSMALTFDP-----YSGACFPITNFLYVKT 675

Db 418 RAE-TPKELANALLGTYVTE-TKSNGFVNTFKPKPVKELYKANOTVALTSNTYKG 473

Qy 676 HLAVQDALL-----SQCICVYFGSQV-----EGRNFRNQFQPVLRRRFYD 717

Db 474 NQEITGETLTKEDXDTGNESQKAETFLTAKINGQAVKWSREAK-----TEL 526

Qy 718 FNGGGFISTRSTRSTVLSSE-GPVSAPNTLQG-----DAPAGRTFOODLARVSV-----764

Db 527 VRGTAKADETVTLALDEKNCVAKHAINEFWQEETKAPEGYLTDDTKTPSISKKVDNNE 586

Qy 765 ---VDIRIVKNRYV-----PGNCNTNLSEAM-----RARLUGLASAYQOEKR 805

Db 587 KNVITTDVTAKEQVTRGFDFKPKLGSDADTAETFDNLSFKVSLEGTXEITGAEKA 646

Qy 806 VDMLHAGLF-----LIKQFHGLLPFGM-----PNNSKS-----PNP 838

Db 647 TTACNEQLGFDSYKGPKENPGLYDYLJEEIA-----PEGFQKITPLEIRSTFKENKDQYAKS 703

Qy 839 QWFWTLLQRNO-----MPADKLTHEITIAVTRFTEYAAVTRF-----FSVSLNRMLYDLPKEKEDSLS 754

Db 704 EVUTTIEEGQXQPIMVNTVPEKLNN-----VLRKSVIYNVY 853

Qy 889 LAQFYMANLILKYCDSQYINTLTSTITGARRPRDPSSVHLWIRD-----VTSAAIDIETQ 945

Db 755 LATWDENKCNLTDFTB-LVDKL-----RYNHEIKDWYVAQALIVEA-799

Qy 946 AKALLEKTENLPELWTAFTST-----HYVRAMNORMPMVVLGJISISKYHGA 992

Db 800 TKAQOEKDEKARPVVIAETTATLANEKGTGTWKILKLTAEQ-----VLRKSVIYNVY 853

Qy 993 AGNNRVIQAGNWGLNGGRNVCPFTGPRGGFICPVTGSSGNRETFLSD 1052

Db 854 YENKVAPAGNE-----PVA-----KDSLNN 875

Qy 1053 QVRGIVTSGGANVQLLAIYATVRAVBAR-----AQEMAFFDMWLSLTDBBEFLARDL--1102

Db 876 QQQ-----TVCNTERTVITQTKAHLEDQSQTTHGVDMDFTDVLD 923

Qy 1103 --BELHDPQIQLTETPTVGEALEAKTILDE-----KUTAGD-----GETPTNLAFNFD 1149

Db 924 GSREAAFTTIALLPDTNKRKTIWKSKEIEHVNDKEFTKTVLAEKDTGKTPGTRKFTF-982

Qy 1150 SSEPSPHTTSNV-----INISGNSISGTVPLKRPEDDE

Db 983 -TEINTVKDQGNTNGKHINEDLKSKQSLTPKRVPTIPSTPXEPE 1024

RESULT 7
 US-09-134-000C-5764
 Sequence 5764, Application US/0913400C
 Patent No. 6617156
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FACALIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 PRIORITY APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: Patent in version 3.1
 SEQ ID NO: 5764
 TYPE: PCT
 ORGANISM: Enterococcus faecalis
 US-09-134-000C-5764

Query Match 1.9%; Score 122; DB 4; Length 1096;
 Best Local Similarity 18.5%; Pred. No. 0.02;
 Matches 208; Conservative 149; Mismatches 410; Index 360; Gaps 53;

Qy 250 RVRNVTAVARGAAHLADEFNENHEGAVLPPDITYTYFOSSSSGTTARGARRNDVNSTS KPS 309

Db 89 RTTSVYAEINGAKQTVFC-TEPGVSIPTETGY-----QRNP 104

Qy 310 PSGGFERRASIM-AADTAHALVIENTGIVEE-----TPTDIKEWPMFI 353

Db 105 PSMDSKAKVSVSLWEKAQTDIDTNNAVAQCMWVNGYKLHSIKRGLGASVDIK-----158

Qy 354 GMGETLPLRNALGSYTA-----VAGTG-ANVFSNPSALVLTEDSGMTBAKOGGP 405

Db 159 SIEGKINK-AIEEYOKKPSFHNTTVKTIGOSTTLIDKNELNISEFKVQNTA-----211

Qy 406 GPSFNRFYOFAGPHIAANPOTDRDGHVLSSQSTGSSNTFSVYDYLICFGAPILLRL 465

Db 212 ---NIDVYRIGNQLVLT-----NSNSKSGTTLIKKIDKESEGVDTKGTGP-VAYKK 251

Qy 466 FYLERCDAGAFTGGHGDALKYVTGSTFDSIIPCSCEKTRTRPVCAHTTVHLRQRMPREGQ 525

Db 252 AGLQTVWAGALDKPPTYAKIKINVERTKGS-LKIKIDKESEGVDTKGTGP-DGK 304

Qy 526 A-----TROPIGVFGTMNSQYSPCDPLOGNYA-----PYLLRKPGDQEAAKATM 570

Db 305 ALPSKDVTDKDGI-----SILDGIPHGTKVTEKSYPDPWMIDTPMAAIIKAGETI 358

Qy 571 QDTYTRATLBFIDLEQERLDRGAPCSSEGSL-----SVIVDHP-----FRBLDILRA 621

Db 359 SMTSKOMRQGQNLKETKG-VETGTDLNNDYSLAGNTPAIRDSPANBIVQETTDEKG 417

Qy 622 RIEQTTOFMKVLYETRDYKIREG-----SEATHSMALTFDP-----YSGACFPITNFLYVKT 675

Db 418 RAE-TPKELANALLGTYVTE-TKSNGFVNTFKPKPVKELYKANOTVALTSNTYKG 473

Qy 676 HLAVQDALL-----SQCICVYFGSQV-----EGRNFRNQFQPVLRRRFYD 717

Db 474 NQEITGETLTKEDXDTGNESQKAETFLTAKINGQAVKWSREAK-----TEL 526

Qy 718 FNGGGFISTRSTRSTVLSSE-GPVSAPNTLQG-----DAPAGRTFOODLARVSV-----764

Db 527 VRGTAKADETVTLALDEKNCVAKHAINEFWQEETKAPEGYLTDDTKTPSISKKVDNNE 586

Qy 765 ---VDIRIVKNRYV-----PGNCNTNLSEAM-----RARLUGLASAYQOEKR 805

Db 587 KNVITTDVTAKEQVTRGFDFKPKLGSDADTAETFDNLSFKVSLEGTXEITGAEKA 646

Qy 806 VDMLHAGLF-----LIKQFHGLLPFGM-----PNNSKS-----PNP 838

Db 647 TTACNEQLGFDSYKGPKENPGLYDYLJEEIA-----PEGFQKITPLEIRSTFKENKDQYAKS 703

Qy 839 QWFWTLLQRNO-----MPADKLTHEITIAVTRFTEYAAVTRF-----FSVSLNRMLYDLPKEKEDSLS 754

Db 704 EVUTTIEEGQXQPIMVNTVPEKLNN-----VLRKSVIYNVY 853

Qy 889 LAQFYMANLILKYCDSQYINTLTSTITGARRPRDPSSVHLWIRD-----VTSAAIDIETQ 945

Db 755 LATWDENKCNLTDFTB-LVDKL-----RYNHEIKDWYVAQALIVEA-799

Qy 946 AKALLEKTENLPELWTAFTST-----HYVRAMNORMPMVVLGJISISKYHGA 992

Db 800 TKAQOEKDEKARPVVIAETTATLANEKGTGTWKILKLTAEQ-----VLRKSVIYNVY 853

Qy 993 AGNNRVIQAGNWGLNGGRNVCPFTGPRGGFICPVTGSSGNRETFLSD 1052

Db 854 YENKVAPAGNE-----PVA-----KDSLNN 875

Qy 1053 QVRGIVTSGGANVQLLAIYATVRAVBAR-----AQEMAFFDMWLSLTDBBEFLARDL--1102

Db 876 QQQ-----TVCNTERTVITQTKAHLEDQSQTTHGVDMDFTDVLD 923

Qy 1103 --BELHDPQIQLTETPTVGEALEAKTILDE-----KUTAGD-----GETPTNLAFNFD 1149

Db 924 GSREAAFTTIALLPDTNKRKTIWKSKEIEHVNDKEFTKTVLAEKDTGKTPGTRKFTF-982

Qy 1150 SSEPSPHTTSNV-----INISGNSISGTVPLKRPEDDE

Db 983 -TEINTVKDQGNTNGKHINEDLKSKQSLTPKRVPTIPSTPXEPE 1024

RESULT 7
 US-09-134-000C-5764
 Sequence 5764, Application US/0913400C
 Patent No. 6617156
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FACALIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 PRIORITY APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: Patent in version 3.1
 SEQ ID NO: 5764
 TYPE: PCT
 ORGANISM: Enterococcus faecalis
 US-09-134-000C-5764

Query Match 1.9%; Score 122; DB 4; Length 1096;
 Best Local Similarity 18.5%; Pred. No. 0.02;
 Matches 208; Conservative 149; Mismatches 410; Index 360; Gaps 53;

Qy 250 RVRNVTAVARGAAHLADEFNENHEGAVLPPDITYTYFOSSSSGTTARGARRNDVNSTS KPS 309

Db 89 RTTSVYAEINGAKQTVFC-TEPGVSIPTETGY-----QRNP 104

Qy 310 PSGGFERRASIM-AADTAHALVIENTGIVEE-----TPTDIKEWPMFI 353

Db 105 PSMDSKAKVSVSLWEKAQTDIDTNNAVAQCMWVNGYKLHSIKRGLGASVDIK-----158

Qy 354 GMGETLPLRNALGSYTA-----VAGTG-ANVFSNPSALVLTEDSGMTBAKOGGP 405

Db 159 SIEGKINK-AIEEYOKKPSFHNTTVKTIGOSTTLIDKNELNISEFKVQNTA-----211

Qy 406 GPSFNRFYOFAGPHIAANPOTDRDGHVLSSQSTGSSNTFSVYDYLICFGAPILLRL 465

Db 212 ---NIDVYRIGNQLVLT-----NSNSKSGTTLIKKIDKESEGVDTKGTGP-VAYKK 251

Qy 466 FYLERCDAGAFTGGHGDALKYVTGSTFDSIIPCSCEKTRTRPVCAHTTVHLRQRMPREGQ 525

Db 252 AGLQTVWAGALDKPPTYAKIKINVERTKGS-LKIKIDKESEGVDTKGTGP-DGK 304

Qy 526 A-----TROPIGVFGTMNSQYSPCDPLOGNYA-----PYLLRKPGDQEAAKATM 570

Db 305 ALPSKDVTDKDGI-----SILDGIPHGTKVTEKSYPDPWMIDTPMAAIIKAGETI 358

Qy 571 QDTYTRATLBFIDLEQERLDRGAPCSSEGSL-----SVIVDHP-----FRBLDILRA 621

Db 359 SMTSKOMRQGQNLKETKG-VETGTDLNNDYSLAGNTPAIRDSPANBIVQETTDEKG 417

Qy 622 RIEQTTOFMKVLYETRDYKIREG-----SEATHSMALTFDP-----YSGACFPITNFLYVKT 675

Db 418 RAE-TPKELANALLGTYVTE-TKSNGFVNTFKPKPVKELYKANOTVALTSNTYKG 473

Qy 676 HLAVQDALL-----SQCICVYFGSQV-----EGRNFRNQFQPVLRRRFYD 717

Db 474 NQEITGETLTKEDXDTGNESQKAETFLTAKINGQAVKWSREAK-----TEL 526

Qy 718 FNGGGFISTRSTRSTVLSSE-GPVSAPNTLQG-----DAPAGRTFOODLARVSV-----764

Db 527 VRGTAKADETVTLALDEKNCVAKHAINEFWQEETKAPEGYLTDDTKTPSISKKVDNNE 586

Qy 765 ---VDIRIVKNRYV-----PGNCNTNLSEAM-----RARLUGLASAYQOEKR 805

Db 587 KNVITTDVTAKEQVTRGFDFKPKLGSDADTAETFDNLSFKVSLEGTXEITGAEKA 646

Qy 806 VDMLHAGLF-----LIKQFHGLLPFGM-----PNNSKS-----PNP 838

Db 647 TTACNEQLGFDSYKGPKENPGLYDYLJEEIA-----PEGFQKITPLEIRSTFKENKDQYAKS 703

Qy 839 QWFWTLLQRNO-----MPADKLTHEITIAVTRFTEYAAVTRF-----FSVSLNRMLYDLPKEKEDSLS 754

Db 704 EVUTTIEEGQXQPIMVNTVPEKLNN-----VLRKSVIYNVY 853

Qy 889 LAQFYMANLILKYCDSQYINTLTSTITGARRPRDPSSVHLWIRD-----VTSAAIDIETQ 945

Db 755 LATWDENKCNLTDFTB-LVDKL-----RYNHEIKDWYVAQALIVEA-799

Qy 946 AKALLEKTENLPELWTAFTST-----HYVRAMNORMPMVVLGJISISKYHGA 992

Db 800 TKAQOEKDEKARPVVIAETTATLANEKGTGTWKILKLTAEQ-----VLRKSVIYNVY 853

Qy 993 AGNNRVIQAGNWGLNGGRNVCPFTGPRGGFICPVTGSSGNRETFLSD 1052

Db 854 YENKVAPAGNE-----PVA-----KDSLNN 875

Qy 1053 QVRGIVTSGGANVQLLAIYATVRAVBAR-----AQEMAFFDMWLSLTDBBEFLARDL--1102

Db 876 QQQ-----TVCNTERTVITQTKAHLEDQSQTTHGVDMDFTDVLD 923

Qy 1103 --BELHDPQIQLTETPTVGEALEAKTILDE-----KUTAGD-----GETPTNLAFNFD 1149

Db 924 GSREAAFTTIALLPDTNKRKTIWKSKEIEHVNDKEFTKTVLAEKDTGKTPGTRKFTF-982

Qy 1150 SSEPSPHTTSNV-----INISGNSISGTVPLKRPEDDE

Db 983 -TEINTVKDQGNTNGKHINEDLKSKQSLTPKRVPTIPSTPXEPE 1024

RESULT 7
 US-09-134-000C-5764
 Sequence 5764, Application US/0913400C
 Patent No. 6617156
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FACALIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 PRIORITY APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: Patent in version 3.1
 SEQ ID NO: 5764
 TYPE: PCT
 ORGANISM: Enterococcus faecalis
 US-09-134-000C-5764

Query Match 1.9%; Score 122; DB 4; Length 1096;
 Best Local Similarity 18.5%; Pred. No. 0.02;
 Matches 208; Conservative 149; Mismatches 410; Index 360; Gaps 53;

Qy 250 RVRNVTAVARGAAHLADEFNENHEGAVLPPDITYTYFOSSSSGTTARGARRNDVNSTS KPS 309

Db 89 RTTSVYAEINGAKQTVFC-TEPGVSIPTETGY-----QRNP 104

Qy 310 PSGGFERRASIM-AADTAHALVIENTGIVEE-----TPTDIKEWPMFI 353

Db 105 PSMDSKAKVSVSLWEKAQTDIDTNNAVAQCMWVNGYKLHSIKRGLGASVDIK-----158

Qy 354 GMGETLPLRNALGSYTA-----VAGTG-ANVFSNPSALVLTEDSGMTBAKOGGP 405

Db 159 SIEGKINK-AIEEYOKKPSFHNTTVKTIGOSTTLIDKNELNISEFKVQNTA-----211

Qy 406 GPSFNRFYOFAGPHIAANPOTDRDGHVLSSQSTGSSNTFSVYDYLICFGAPILLRL 465

Db 212 ---NIDVYRIGNQLVLT-----NSNSKSGTTLIKKIDKESEGVDTKGTGP-VAYKK 251

Qy 466 FYLERCDAGAFTGGHGDALKYVTGSTFDSIIPCSCEKTRTRPVCAHTTVHLRQRMPREGQ 525

Db 252 AGLQTVWAGALDKPPTYAKIKINVERTKGS-LKIKIDKESEGVDTKGTGP-DGK 304

Qy 526 A-----TROPIGVFGTMNSQYSPCDPLOGNYA-----PYLLRKPGDQEAAKATM 570

Db 305 ALPSKDVTDKDGI-----SILDGIPHGTKVTEKSYPDPWMIDTPMAAIIKAGETI 358

Qy 571 QDTYTRATLBFIDLEQERLDRGAPCSSEGSL-----SVIVDHP-----FRBLDILRA 621

Db 359 SMTSKOMRQGQNLKETKG-VETGTDLNNDYSLAGNTPAIRDSPANBIVQETTDEKG 417

Qy 622 RIEQTTOFMKVLYETRDYKIREG-----SEATHSMALTFDP-----YSGACFPITNFLYVKT 675

Db 418 RAE-TPKELANALLGTYVTE-TKSNGFVNTFKPKPVKELYKANOTVALTSNTYKG 473

Qy 676 HLAVQDALL-----SQCICVYFGSQV-----EGRNFRNQFQPVLRRRFYD 717

Db 474 NQEITGETLTKEDXDTGNESQKAETFLTAKINGQAVKWSREAK-----TEL 526

Qy 718 FNGGGFISTRSTRSTVLSSE-GPVSAPNTLQG-----DAPAGRTFOODLARVSV-----764

Db 527 VRGTAKADETVTLALDEKNCVAKHAINEFWQEETKAPEGYLTDDTKTPSISKKVDNNE 586

Qy 765 ---VDIRIVKNRYV-----PGNCNTNLSEAM-----RARLUGLASAYQOEKR 805

Db 587 KNVITTDVTAKEQVTRGFDFKPKLGSDADTAETFDNLSFKVSLEGTXEITGAEKA 646

Qy 806 VDMLHAGLF-----LIKQFHGLLPFGM-----PNNSKS-----PNP 838

Db 647 TTACNEQLGFDSYKGPKENPGLYDYLJEEIA-----PEGFQKITPLEIRSTFKENKDQYAKS 703

Qy 839 QWFWTLLQRNO-----MPADKLTHEITIAVTRFTEYAAVTRF-----FSVSLNRMLYDLPKEKEDSLS 754

Db 704 EVUTTIEEGQXQPIMVNTVPEKLNN-----VLRKSVIYNVY 853

Qy 889 LAQFYMANLILKYCDSQYINTLTSTITGARRPRDPSSVHLWIRD-----VTSAAIDIETQ 945

Db 755 LATWDENKCNLTDFTB-LVDKL-----RYNHEIKDWYVAQALIVEA-799

Qy 946 AKALLEKTENLPELWTAFTST-----HYVRAMNORMPMVVLGJISISKYHGA 992

Db 800 TKAQOEKDEKARPVVIAETTATLANEKGTGTWKILKLTAEQ-----VLRKSVIYNVY 853

Qy 993 AGNNRVIQAGNWGLNGGRNVCPFTGPRGGFICPVTGSSGNRETFLSD 1052

Db 854 YENKVAPAGNE-----

354 GMEGLPLRNALGSYTA-----VAGVIG-AMVFSNPNSALYLTVEEDSGNTTEAKDGGP 405
 Qy :|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|:
 Db 181 STEGKINK---AIEEYQKKSFSFNTTVDLQNLNSELFDKVVONTA---- 233
 Qy 406 GPSPNRFYOFAGPHILAAANPOTDRDGHVLSSOSTGSSNTFSDYTLICFGQFAPILLRL 465
 Db 234 ---NIDYRIVGNQLVTP-----NSNSKGTLTKEGATGTP-VAYK 273
 Qy 466 FYLERCDAGAFTGGHGDALKYVTGTFDSRIPCSU---CEKHTRPVCAHTTYVHLRQMRP 521
 Db 274 AGLOQITVMAGALDKNTYAK-----IDVETKGSKIRKIDKESGDIVPETYFL----- 322
 Qy 522 RFGQA----TROPIGVFTMNSQYSDCDPLGNYA-----PYLLIRKPGDQEAA 566
 Db 323 DFGKALPSKDVTTDKDG-----SILQDIPHGTKVTTIEKSVDPYMDITTPMAATKA 376
 Qy 567 KATMODYTATLERLFIDIEQERLILDRGPSCSSEGSL-----SVIHDPT--FRIILD 617
 Db 377 GETISMSTSKMRQGQILLEKTG-VETGNDLNNSLAGNTFAIRDSPAGEIVQBITM 435
 Qy 618 TLRARIEQTTOFPMKVLYTRDYLIREGSEATHSMALDFD-----YSGAFCPITNF 671
 Db 436 DEGRAB--TPKELANALLGLTYVTE-TKSGNGFINTFKPTKVELKYANOTVALYTSN 491
 Qy 672 VKRTHLAVYQDIAL-----SQCHCWFYQGQV-----EGRNFRNQFQPVLR 713
 Db 492 VKGQNQETITGETTLTKEDDTGNESSQGKAEYLTAKDQAVKNSWAEK----- 545
 Qy 714 FVDLFNGGGTSSTRSITVILSE-GPVSAAPNTLQ-----DAPAGRFFGDYLARYSVE- 764
 Db 546 -TELVKGTASDETKASDETKASDETKASDETKASDETKASDETKASDETKASDETK 604
 Qy 765 -----VIRDIVRGNRVV-----PSGNTNLSEAA-----RARLVGLASAYQR 801
 Db 605 DNNEKNNAV1TRDVAKEQVIRFGDFEFKAGSDGTAETGENDLSFVSPLEGTEIN 664
 Qy 802 QEKRVDMLHGAF-----LHQQFHGLLPRGM-----PNSNKS----- 835
 Db 665 EDAKATTACNEQLGFDGYGKFENLPYGDYLLIEEA--PEGFOKITPLEIRSTPKENKDD 721
 Qy 836 -PNPONWETLQRNQ-----MPADKLTHETTTIAKVEETTAINFNLNP--PT 884
 Db 722 YAKSVEVFITTEBQKQPTKMTVTPYEKLTNN-----FSVSINRMLMEYDLPKED 772
 Qy 885 CIGELAQFYMANLILKCYCDSQYLIINTLTSITGARRPRDSSVILHTRKD---VTSAAD 941
 Db 773 SLTSLATWDGNGKLNLTIFTE-LNDKL-----RYNLHELKEPDYVVAIAID 818
 Qy 942 IETOAKALLEKTNLEPEMLTTAFTST-----HYLAAMNQRMVPMVLGISISK 988
 Db 819 VEA-TKAQEEKDEAKPVVIAETTALANKETGTWKHLKLTAEQ-----VLDKSVL 871
 Qy 989 YHGAAGNNKVKVQAGKVGSGLINGGRNCVPLFEDTRFLIACPRGGFICPVTGPSSGRET 1048
 Db 872 ENYYENKVAPEAGNE-----PVA-----KDA 893
 Qy 1049 TLSDOYRGITIVSGGAMVQLAIYATVRAYGAR-----ACMNAFDWLSTSUDDEFALAR 1100
 Db 894 SLMNQDQ-----TMVNC TIERHSIQTAHEDSGQTETHGMDMDDGWT 941
 Qy 1101 DL----EELHDQIOTLQLETPWTVGCALEAKVILDE-----KTTAGD---GETPTNLA 1145
 Db 942 DVLDSSKEAFETIYLALLPDGTNKEIWKGKIEBEVNDKEFTRVLAKEVDTGKYPBTGK 1001
 Qy 1146 ENFDSCEPSEHDTTSNV-----LNISSGNSISSTVPGKLRPPDDE 1185
 Db 1002 FTF--TEINYEKGDNVNGKHNEDIKEKSOTLTPKEVTPSTPKQPE 1046

RESULT 8
 US-09-252-991A-16913
 Sequence 16913, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfeld et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIORITY FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIORITY FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 16913
 ; LENGTH: 370
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-16913
 ; Query Match Score 118 5; DB 4; Length 370;
 ; Best Local Similarity 20 2%; Pred. No. 0_0061;
 ; Matches 93; Conservative 46; Mismatches 137; Indels 185; Gaps 19;
 ; Query 208 PDPENTHRSIGEGTVYPIBPYNTGCLHIDTCVTAPEVALVRNTAVARGAHLAPD 267
 ; Db 17 PDPCCNAYH-----TDEQRWAALTRD 37
 ; Query 268 ENHEGA-VLPPDITYTQFQSSSGTTARGARNVN-SSTSKEPSGGB-----BR 316
 ; Db 38 AAADGFVYVAKTGTGVCYCRPSS---ARRPRRNVEFFATAEEAAGYRPSRSAAGDR 93
 ; Query 317 RLASTMAADTALHAETVINFNTGIYEPPTDIKEWMFMIGHE-----GTLPRLNA 364
 ; Db 94 RLAABEGRERAERVAQACRMIET-----ETPPALEALARLGMSPPFHRLFKAETGLTPKAYA 150
 ; Query 365 LGSYTARVAGYIGANVFSNPNALYTIVEDSGMTEAKDGGPFEFNRFQFAGHLLAAMP 424
 ; Db 151 SAYRARLREBLRQGQASASVTEAIY-----DSGFN-----SNRSPYESSSRGLRNP 196
 ; Query 425 QTDRDGHVLSQSTGSNTESFSDYLAICFGFAPLALARLFLYLERCDAGAFTGGHGDAL 484
 ; Db 197 RDYRDG-----GAG---AIRFAIGQCSLGAI-----220
 ; Query 485 KYVTGTFDSEIPCSLQEKHTRPVCA-----HTTVHLRQLRQMPR-----FGQATR 528
 ; Db 221 -----LVAQOSORGICALLGEPEPELRELQDOPRAOLGGDADFERLYA 266
 ; Query 529 QPIGVFGTMNSQYSDQPLNAYPLILRKPGDQTEAKATMQ-----DTYRATLRF 582
 ; Db 267 QVVG-----EVESPQLGLDLP-LDVYRTGAFQERVQWQALREIPPGSTASYAQIAERI- 316
 ; Query 583 IDLEQERLDRGAP-----CSESEGILSSVYDHPTRR 614
 ; Db 317 -----GAPRVRVAQACANRIVAVPCHRVR 346

RESULT 9
 US-09-489-039A-12681
 ; Sequence 12681, Application US/09489039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709-2004-001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; PRIORITY FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO: 12681
 ; LENGTH: 855
 ; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae
 us-09-489-039A-12681

Query Match 1.9%; Score 117; DB 4; Length 855;
 Best Local Similarity 21.8%; Pred. No. 0.042;
 Matches 107; Conservative 54; Mismatches 140; Indels 190; Gaps 29;

Qy 320 SIMA----ADTAHAEVINTGTYBETPDIKEWPMFIGMEGTPLRNLGYTARYAG 374
 Db 240 SIMAFGDNTDSSLFGSLSSN-GI-KLATDERMWPO-GKRGYAPEVHGVAASSARV-- 292

Qy 375 VIGAMVFSPLSALVTEVEDSGMTEAKDGGPGP---SFNRFFQ--- 414
 Db 293 ---VIQLQGKVIVTHVP-----PGPFYIDDLINTRYQDLOVKVBANGKVS 337

Qy 415 -FAGPHFLANPOTDGD-----HVLSSQSTGSNTES 446
 Db 338 RFTVY-SAYDSVREGNMYIAFAFGKVCYORYIDNRFLEGTLOHGVNNHLTLNGLSIA 396

Qy 447 VDYLALICGCGAPLLARLLFYLERDAGAF-----TGG-HCD 482
 Db 397 HDYQAWLA--GGVLATRL-----GAFGMNATWSGAQVEERNDROQCMRAEFSYSKTF 445

Qy 483 -----ALKYVGTF-SEIPEPSL-CRKHTREVCAITVHLRQMRPFCQATROP 531
 Db 446 STGTINLVLAAYRSYSGPRLDEDYFGVRQCEHNSIVYSTDHQ-RQL---SATVSPL 501

Qy 532 GVFGTMTNSQYSDCPIGNTAP-----YLIRK 558
 Db 502 GRILGNLSASTADYNNRKRITQIQLQGINSQNWKVSYCENLARQSTSDDGFYHSCNE 561

Qy 559 PGDOTEAAKATMODYTATLERLF-----IDLEQFRLLDRGAPCSSEG----- 601
 Db 562 PQDINQRQKTT-ETTLSFTSIPPNWGDNNTSVANNYNOSR-ANRSTSLSMNTRGEONE 619

Qy 602 LS-STVUDHTFRR---JIDTLRARIETQTQFMKVLU---ETRDYK---IREGLSRAT 650
 Db 620 LSWSYGGVYRNQYNGDEGTTATGGNVQO-NTRFGALRYCYDQSKDYQVALSSGSVVL 678

Qy 651 HSMLATFDPKS 661
 Db 679 HSGGTTFGPRA 689

RESULT 10
 US-03-091-609-2
 ; Sequence No. 0000029
 ; GENERAL INFORMATION:
 ; APPLICANT: SHERMAN, DAVID H.
 ; APPLICANT: WILLIAMS, MARK D.
 ; APPLICANT: XUE, YONGQUAN
 ; TITLE OF INVENTION: METABOLIC ENGINEERING OF POLYHYDROXYALKANATE MONOMER SYNTHASES
 ; FILE REFERENCE: 600.297US2
 ; CURRENT APPLICATION NUMBER: US/09/031,609
 ; CURRENT FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: PCT/US96/20119
 ; EARLIER FILING DATE: 1996-12-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 4630
 ; TYPE: PRT
 ; ORGANISM: Streptomyces venezuelae
 us-09-091-609-2

Query Match 1.8%; Score 111; DB 4; Length 4630;
 Best Local Similarity 19.7%; Pred. No. 4.2;
 Matches 250; Conservative 109; Mismatches 419; Indels 494; Gaps 66;
 Qy 51 NLTVKETFTSSIAVV-----SGARTTGLAGAGITKLKTSHFVPSVFTFHGGKHKVLP 102
 Db 166 SULTVDAQSSSLVAVLACESURAGESSTTALV-AGVNL-----NLIA 206
 Qy 103 SSAAPNLTACNAARERFGFSRCQGPVDGAVETTSAEICUQLGLEPENTLYLVVTAFL 162
 Db 207 ESA-----VTEERFG-----GLSPDGAYTFDARA-- 231
 Qy 163 XEAVFMCNVFLHYGGDLDIVHINHGDTYRIPLFPVQFMPDVNRLYVPDFNTTHRSIGEGF 222
 Db 232 -----NGFREGEG-----GIVVTLKPL-----SRALADDGRVH---GV 261
 Qy 223 VYPTPYFTNTGLCHLHDICVIAPIVAVLVRVNTVAYARGAHLAFAFDENHEGAVLPPDITYT 282
 Db 262 IRASAVNNDG-----ATEGITVPERAAQEVLRAYRAKALDPS-AVQ 303
 Qy 283 YFQSSSGTGTARGARRNDVNTSKSPSGCFERRASIMAAATLHAEVFNTGJIYET 342
 Db 304 YELTHHGTT-----PVGDPLEAAALGAVLGSGARADEPL-----LVGSA 342
 Qy 343 PTDIKEYPMFIGMEGTIPRNALGSYTARVAVGIVANVSPNSALVYLTVEVDGSMTEAKD 402
 Db 343 KTNVGHLEGAGIVGLIKTLLALG-RRIPASLNFRTPHDPL-----DTLGDVPD 394
 Qy 403 GSGPSPSNRFRYQAGPHIILAANPQTDRD-----GHVLLSQSTSSSNTEFSVSD 448
 Db 395 G-----LREVPHPDRELLLAGVSSFGMGGTNAHVVLSEPAQGGBOPGID 438
 Qy 449 YLALICGFGAPIPLJFYLERDCAGA-----FTGGBGDALK-----YVTGTFDSEI-P 496
 Db 449 EETPV-----DGAALPPVVTGGEARAAQARRLHEAVEADPELAP 480
 Qy 497 CS1CEK--HTRPVCAHTV-----HRLRORMPRFGQATOPIQFVGTMNSQYSDCDPLG 548
 Db 491 AALARSLSVTTTRVETHRSVLAIDPDRARLLDGLGALLAGTAPGVWTGT----- 528
 Qy 549 NYAPYLLRKPGDQTEAKATMDTYTATLERLFIDLEQERLLDRAPCSSEGSSLYTVD 608
 Db 529 -----PAPG-----RLAVLF-----SGQQAQRTANGM-TLYAA 555
 Qy 609 HPTFERRLDUTPARIETTTQFMKVLUETRD-----YKTRREGLSBATHSMALT 656
 Db 556 HAPATAFDAVAELDLDPLAELVAAQDTLDRTVHTOPALFAYEVHLRVEWSVGT 615
 Qy 657 FDPSGAFCPITNFLYERTHLLAVVQDIALSQCCHCVFYQQVQEGRNFRNOFOFVLRFFVD 716
 Db 615 PDLLAGH---SVGEISAAHVAGV--LSSLRDA-----ARLVAARGRLMQALP----- 656
 Qy 717 LFNGGFISTRSTVTSSEGPSAQNPTLGODAAGTDFGDLARYSVEVIRVNRVV 776
 Db 657 --EGGAM---VAVEABEEVL---PHL---AGBRELSLAVN-----GPPAVV 694
 Qy 777 FSGNCNTNSEAARARVGLASAYQRQEKVDMHLHGAGFLKQFHGSLF----- 825
 Db 695 LAG-----AERAVDLYELLREQGRKTRKLSVSHA-----FHBLMBNLDDRRVV 741
 Qy 826 -----PR-----GMPNPKSPNQW---FWTLLQRNOMPADKLTHEBTIAAV 866
 Db 742 EELDFQFRDVYVSTVGLPVA---GQNTDPEW-----VDOV-RRPVRFLDAV 787
 Qy 867 KRTEEEAAINFINLP---TCIGELAFCYMANLILKCDHQYLNTLTSITGARRPD 924
 Db 788 -RTLEESGADTLELGDGVCSAMADS-----RQEAAATAVSALARKG--RP-E 833
 Qy 925 PSSVLMHTRKDVTSAADIETOQAKALLETKENLPELWTAFTSTHLYRAAMNQRPMVTLGI 984
 Db 844 POSLAAAGTIVVRGHAVD-----WTAHHSSTGTIVRVL-----PTYAFQR 874
 Qy 985 SISKYHAGAAGNVRQAGNWGLNGGNCVNPCLFETDRTRRFIACPRGGFICCPVTPGSSG 1044
 Db 875 ERHWDGAAARTAAAPLTAAGR-SGTGAG-----TGPAG 905
 Qy 1045 -----NREITLSDQURGIIIVSGAMVQIAIYATVRA-VGARA 1081

RESULT 11
US-09-105-537-2

Sequence 2, Application US/09105537A

Patent No. 6265202

GENERAL INFORMATION:

APPLICANT: Sherman, D.H.

APPLICANT: Liu, H.

APPLICANT: Xue, Y.

APPLICANT: Zhao, L.

TITLE OF INVENTION: DNA encoding methymycin and pikromycin

FILE REFERENCE: 600 438US1

CURRENT APPLICATION NUMBER: US/09/105,537A

CURRENT FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 5215

TYPE: PRT

ORGANISM: Streptomyces venezuelae

US-09-105-537-2

Query Match Score 1.8%; Score 111; DB 3; Length 5215;
Best Local Similarity 19.7%; Pred. No 5.2; Mismatches 109; Indels 494; Gaps 66; Matches 250; Conservative 109;

Qy 51 NLTVKTFSSLAVV-----SGARTGLAGAGITKLTKTSHFYPSSVFVFGGKREVL P 102
Db 166 SLTVIDAQSSLVAHLACESLRAGESTALV_AVGNL-----NILA 206
Qy 103 SSAAPNLTRACNAAEREFCSRCQQGPYDGAETTGAEICTRGLEPENTILLYWVTPALF 162
Db 207 ESA-----VTEBERFG-----GLSPDGTAYTEDARA- 231
Qy 163 KEAVFCNCVPHHYGGLDITHINHGDIYRPLPPIQLEMDVARYLPDPFNTNHRSIGGF 222
Db 232 -----NGFVRGEG-----GGTVVNLKPL-----SRALADGRVH----GV 261
Qy 223 VYPTPYNTGLCHLTHDCVIAVMAVALRVNTVAVARGAHLAEDNEEGAVLPPDITYT 282
Db 262 TRASAVNDG-----AFLGLTVPSRAQEKTREAARKAALDPS-AVQ 303
Qy 283 YFQSSSSGTTARGARRNDVNSTSCKPSPGCFERLASMIAADTALHAEVINTGIYET 342
Db 304 YVELHGTGT-----PVGDPBIEAALGAVLGSRAPADEPL-----LVCSA 342

Qy 497 CSLCEK- HTRPVCAHTV-----HRLRORMPRFGQTROPIGVFGTMNSQYSDDCPLG 548
Db 481 AALRSLLVTRTVPFRSYLAPDRRLIDGLGALAATPAPGVVTGT----- 528
Qy 549 NYAPYLILRKPGDQTEAAKATMDTYRATERLFDLEOEIRLDRGAPOSSEGGLSSIVD 608
Db 529 -----PAFG-----RLAVLF-----SCQGAQRTGMGM-EVYAA 555
Qy 609 HPTFRIIDLTUARTEQTTOFMKVLFVTRD-----YKIREELSEATHSMRBLT 656
Db 556 HPAFATAFDAVAEELPDDRPLAEVAGDTLDRTVHTQALFAVEYALHRLVBSWGVY 615
Qy 657 FDPLYGCAFCPITNPFIVKRTHLAVQDALSQCHCVFGQVEGNFRNFQOPVIRRFD 716
Db 616 PDLLAIGH---SVGEISAAHVAGY-LSRDA---ARLVAARGRLQALP----- 656
Qy 717 LFNGGFSIISTRITYLSEGFVSADNPYLGQDAPAGRTEFDGLALARVEVTDIYKRNRYV 776
Db 657 --EGGM-----VAYEASEEFLV--PHL-----AGRERLSSLAVN-----GPAV 694
Qy 777 FSGNCNTNLSEAAARLVLGLASAYOREKRVDMHLGAIGFLKQPHGLLP----- 825
Db 695 LAG-----ARLVAELLREQGRTRKLSVSHA-----FHSPLMBPMLDDFRRVY 741
Qy 826 -----PR-----GMPPNSKSPPNPN-----FWTLQLQRNQNPADKLTHEETTIAN 866
Db 742 EELDFDPRYDVUSTTGLPVTA---GQMTDPEYW-----VDQV-RRPYRFDAV 787
Qy 867 KRFTEYYAAINFNIFP-TCIGELAQFTMANLILKYCDHSQYINTUTTSIITSGARRPRD 924
Db 788 -RTLESQGATDFLEPDGCGSAMRADSV-----RDQEAATAVSALKG-RP_E 833
Qy 925 PSSVLMWIKDVTSAADIEQAKAALLEXTENLPELWTTAFTSTHLVRAAMNORPMVVLGI 984
Db 834 PQSLLUALITYTVFVRSHDVD-----WTAHHSIGTIVRVP-----PTYAFQR 874
Qy 985 SISKVHGAAGNNRVEQAGHNSGLNGSKVNPFLFTRTRBFITACPRGGFICPVTGPSSG 1044
Db 875 ERHWFDGAARTAAPITAGR-SGTGAG-----TGAAG 905
Qy 1045 -----NRZTILSDQVRGTLIVSGGAMVQLAIYATVVRAGARA 1081
Db 906 VTSGBGEGEGEAGAGGGDRPARHETT-ERVRAHVA-----VLEYDDPPTRELGLTF 957
Db 1082 QHMAFDOWLS-----LTDDEFLARDLLEHDQIQTQTLTPWTVEGALAEVKILDEKTTA 1135
Qy 958 KELGPDSLMSVLRNLNVDDTGLRUPSGLFLDH-----PP-----RALLA--HLGDLLTG 1006
Db 1136 GDEGETPNLAFNDSCEPS-HDTTSINVNTSGSNSTSSTVPGLKRPBBDDELFDL----- 1189
Db 1007 GSGETG-----SADGJPPATPADTAEPIALIG--MACRYPGGVTSPEP-LNRLVAEG 1056
Qy 1190 ---SGIPIKHG 1197
Db 1057 RDAVSGJPTDRG 1068

RESULT 12
US-09-543-681A-6059

Sequence 6059 Application US/09543681A
; Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344-09

SEQ ID NO 6059 LENGTH: 790

TYPE: PRT
ORGANISM: *Proteus mirabilis*
US-09-543-681A-6059

TYPE: PRT
ORGANISM: *Proteus mirabilis*
US-09-543-681A-6059

TYPE: PRT
 ORGANISM: Proteus mirabilis
 US-09-543-681A-0059
 Query Match 1.7%; Score 110; DB 4; Length 790;
 Best Local Similarity 19.1%; Pred. No. 0.19;
 Matches 171; Conservative 124; Mismatches 350; Indels 250; Gaps 42;
 PMSIGMECTL-----PRNLALGSYTTARVAGTIGAMVESPNT 384
 PLFVGREKSIHCLEAANNDNKQIMLVAKQDASTDEPGVNDLTS-VGTAVASYLQMLKLKDGS 92
 DY 34 SALYLTE-VEDSGMTEAKGGCGPSFNRFYQFAGPHLAANPOTDRUGHVSSQSQTSSNT 443
 TYKVLVGCIRRKITTLSNG----BYFQKAETLDTPYVDEREQEVINR---TAIN 142
 DDB 93 EFSVDYALICFGAPLLFYLERCDAAGFTGHH-----GDALKY 486
 QFE-GYI KLNKKUPPEVLA SHLAIEESAKLADTIAISMPKLKDQAVLЕНSDUTERLEY 201
 DDB 444 EFSVDYALICFGAPLLFYLERCDAAGFTGHH-----GDALKY 486
 143 QFE-GYI KLNKKUPPEVLA SHLAIEESAKLADTIAISMPKLKDQAVLЕНSDUTERLEY 201
 DDB 487 VTSFEDSRSIPCSCEKHTRPVCAHTTVHLRDRMPR----FGQATRQP/GVFGTMNSQ 540
 202 LMMAMESBIDLLOVERKIR-----NRVKQMKERSQEEYLYNEQMKAIQKELEMDDA 253
 DDB 541 YSPCDPELGNAYAPLILRKPGDQEAAKATMQD-----TYTACDLERLFLIEQERLLDR 593
 PDMEESLRKRKIE-AAKPMEKREKTEALQKURMSPMSAAEATVRSYIOWMVQ----306
 DDB 594 GAPOSSEGIISSVIVDHPTFERRILDTLRARIETQTTQFMKV-----VETRDYKIREGLSRATHS 652
 307 -VPWNSR--SKVRKDLVRAQEVLDTDHYGLERVKERILEYLAQSVRSYIOWMVQ----357
 DDB 653 MALTFDPSG-----AFCPITINFLVURTHLAVQDQLASQCHCVFYGQOQEGRNFRNQ? 706
 DDB 358 LCLVGPPIGYKTSIGQSTAKATGRKYRMALGEVRD-----ELRGH----400
 DDB 707 QPVLRRPFPVLNGGFISRTSTVTLSEG PVSAPNPLG QDAPAGRIFD--GDLARVSV 764
 401 ----RTYIGSMGPKLIOKMA-----KVGYKNPFLFLDEDKNSSDMRGDPASALL 448
 DDB 765 VI---RDIRVKNR-----VVFSGNCNTNLSEPA---RARLVGLASAYQRQEKRVD 807
 DDB 419 VLDEQEQTAFNDHYLEDDLDLSMVFATVNSNNTIPDLDRMEVIL-SGTYTEDK-- 504
 DDB 808 MLHGALGFL-KOPFHGLPRGMNPNSKSPNQFWTLLQRNQMPAKLTHEBTTIAAV 866
 DDB 505 -LNTAKCHLPLKQ-----JERNALKENELTIDSAMGII 538
 DDB 867 KRFTYEYAZINF---NLPTCTIGLAQFYMANLRLKCDHSQVINTLTSITGARRPRD 924
 DDB 539 RYTRE-AGVRSLEREISCKRKAVKQOLMDSTI---KHBIDENNKKDYL-GVRL-- 589
 DDB 925 PSSYLAHWIKRD-----VTSAADIETOAKALLEKTENIPELMWTAFT-STHIVRAAMNQ 976
 DDB 590 ----VDYGRADTERIGHTGLANTEVGDLLTETASWPCKRKTFTGSLFVQMESISQ 645
 DDB 977 RPKMYLGISISKYHGAAGNNRVEQAGNWGLNGGKNVCPLETFDTRTRFFIACPRGFFTC 1036
 DDB 646 AAMTIVRARAIDLK-----GING-----DYEKRDHVHPEGA-T 679
 DDB 1037 PVTGESSGNETT----LSDQURGIIUSGGAMVQLAITYTUVARGA-----AQMF 1086
 DDB 680 PKDGEPSAGTAMCTALVSSLTGPNPVRSDVMTG--EITLRGOVLPICGKKEKLLAHRGG 736
 DDB 1087 DDWLSLTIDDEFARLDELDQIQTLETWVGEALEVKILDEKTTAGDGETP 1141
 DDB 737 IKTWLIPDEN-KRDLEEPIFENIVADL-----IHYVKTIEEVLJALKEESP 781
 DDB 11331 AGPVSYAVADV-DWPVISEGPAATRP-----TALFAILAGR 1365
 DDB 395 SGNTAEKADGGGPSFRFVQFAG-----PHIAANPQTDRDGHVLSOSTGGSNT 444
 DDB 1366 GGOAEAPDS-GPTGEPQAQLGLSPDEQQENLLEVANAYAE---VLGHESAABINVR 1420
 DDB 1421 RAPELGIDSUNAMAJKRL-----SASTG-----LREPASL-----LREPASL
 DDB 505 RPVCAHTTVHLRQ-RMPRFEGOATRQPIGEGTMNSQYSDCDPL-----CNYA 551
 DDB 1442 RESULT 13
 DDB 1443 US-07-642-734C-4
 DDB 1444 Sequence 4, Application US/07642734C
 DDB 1445 Patent No. 8924513
 DDB 1446 -
 DDB 1447 -
 DDB 1448 -
 DDB 1449 -
 DDB 1450 -
 DDB 1451 -
 DDB 1452 -

RESULT 13
US-07-642-734C-4
; Sequence 4 ; Application US/07642734C
; Department NO. 5004513

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/439,009A
 FILING DATE: 11-19-95
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Casucci, Dianne
 REGISTRATION NUMBER: 40,943
 REFERENCE/DOCKET NUMBER: 4952.US.D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-938-3137
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3567 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-439-009A-4

Query Match 1.7%; Score 106.5; DB 3; Length 3567;
 Best Local Similarity 19.9%; Pred. No. 74;
 Matches 237; Conservative 104; Mismatches 384; Indels 465; Gaps 62;

Qy 1567 ITPREALMDPQQLRMLTAAVEAGIDDALRGSTDVFGNGNQSYMOLLAGEER 1626
 Db 1567 KATHDQTYRATLLELFIDLQEERLLDAPCSSEGGSVIVDHPTPR 614
 Qy 615 I-----LDTLRARIEQT-----TTQFMKVILVETRDVKIREGLSEATHSMAL 655
 Db 1627 VDGXOGLNSASVLSGRAYTEFGMEGPALTVDACSSSLVGI-HLMQALRGECSLA 1684
 Qy 656 T-----FDPYSGAFCPTINFVLRKTHAVYQDIALSQCICVFQVQGRNFRN---- 704
 Db 1685 AGGYTVNSDPYI-----FVDFSTQR----GLA-SDRCKASARAGFASEGVYAL 1731
 Qy 705 QFOPVLRRFVDFLNGSFISTSRTSVPASAPNPFLGODAP----RFFGDGLAR 760
 Db 1732 VLEPLSRA-----ANG----HQVLAVLRSAAVNODGASNGLAPNGPQERTVQALA 1782
 Qy 761 VSVVBVIRYKRVYTFSGNTCNLSEAAARARLVGLASAYKORQEKR-----VDMHLH-- 810
 Db 1783 SGVPA-ADVDV--VEAHGTGTELGDPIEAG--ALLATYQDDRDRPLRUSVKINIGHTQ 1836
 Qy 811 -----GALGFULKQPHGLIFPRGNPENPSNPWNFTLQRNOMPDKLTHEITIA 864
 Db 1837 AAAGAAASVIVKUVALMEHGM_PRESHADELSPHDW-----ESGAEVIREEVWPA 1887
 Qy 865 AVKRFTBEYAAINFNIPPTCIGELAQFYMANLILKYCDHSQYLINTLTSITGARRPD 924
 Db 1888 GER---PRAGYSSFGVSGT-----NAHVIVBEEAPEQ-----EAARTERG 1925
 Qy 925 PSSVLHMKDVTSAADIEQOAKALLEKTENLP-----WTAFTSTHL-YRAAMNQR 977
 Db 1926 PLPFVLSGRSEAAVA---QARALAEHRLDTPELGLTDRAWLTGARFDTAAV-- 1978
 Qy 978 PMVVLGTSISKHGAGNNTRYQAGNWISINGGNCPFTFDTRPFLIAPCRGGTICP 1037
 Db 1979 -----LGDDRGAVCAELDAEGR-----PSADAVAP 2005
 Qy 1038 VTGPSSGRRETTLSDVQRLIVLVSAGMQLAIATVVRAGAQAQHMAFFDNLSLTDEF 1097
 Db 2006 VT---BARKPV-----VPGOGAQ-----FVG-----2026
 Qy 1098 LARDLBLEHLDOLIQT-----ETPNVVEGALEYKILDEKTTAGDG 1138
 Db 2027 MARDLLESSEVFAEMSRSRCAEALSPTHDW-----KLLD--VVREGDG 2065

RESULT 14
 US-08-439-009A-4
 Sequence 4, Application US/08439009A
 Patent No. 6004787
 GENERAL INFORMATION:
 APPLICANT: Donadio, S
 CORRESPONDENCE ADDRESS:
 STREET: Abbott Laboratories D377/AP6D-2 One Abbott
 STREET: Abbott Laboratories Park Rd
 CITY: Abbott Park
 STATE: IL
 COUNTRY: US
 ZIP: 60064-2500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

Qy 552 PYLIR-----KPGDQTEAA-----566

Db 1421 RAFSLGDSLNAMETRL-----SASIG-----LRIPLASL----1452

Qy 505 RPVCAHTTWRHQ-RMPRFQGATRDPFQGFTMSQYSDGDP-----GNYA 551

Db 1453 -VEDHPPTUTALAQHLLRVLGDDAQAVRYVGAAD--ESEPIAIVGIGCRFFGGIGS 1506

Qy 552 PYLIR-----KPGDQTEAA-----566

Db 1507 PEQLWVLAEGANLTGPPADRGWDIIRLYHPPDNPNGTSVYDKGFLTDADDFEGFFG 1566

Qy 567 -----KATMDTYRATLERLFIIDLEQERLLDAPCSSEGGSVIVDHPTFRR 614

Db 1567 ITPBEALMDPQQLRMLTAAVEAGIDPALRSTDGTVFGNRNGQSYMQLLGEAER 1626

Qy 615 I-----LDTLRARIEQT-----TTQFMKVILVETRDVKIREGLSEATHSMAL 655

Db 1627 VDGXOGLNSASVLSGRAYTEFGMEGPALTVDACSSSLVGI-HLMQALRGECSLA 1684

Qy 656 T-----FDPYSGAFCPTINFVLRKTHAVYQDIALSQCICVFQVQGRNFRN---- 704

Db 1685 AGGYTVNSDPYI-----FVDFSTQR----GLA-SDRCKASARAGFASEGVYAL 1731

Qy 705 QFOPVLRRFVDFLNGSFISTSRTSVPASAPNPFLGODAP----RFFGDGLAR 760

RESULT 15
 US-07-731-157A-7
 Sequence 7, Application US/07731157A
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Quax, Wilhelmus J.
 ; APPLICANT: Misset, Onno
 ; APPLICANT: Van der Laan, Jan M.
 ; APPLICANT: Lenting, Herman B.M.
 ; TITLE OF INVENTION: Mutated beta-lactam acylase genes
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
 ; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94041
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.26 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/731,157A
 ; FILING DATE: 19910509
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 90200962
 ; FILING DATE: 18 APR 1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER PH.D., BARBARA
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: GBRO-027/000US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-494-7622
 ; TELEFAX: 415-557-0663
 ; TELEX: 380816 COOLBE PA
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 774 amino acids

; TYPE: AMINO ACID
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Pseudomonas species
 ; STRAIN: SE83
 ; US-07-731-157A-7
 ; Query Match Score 1.7%; Length 774;
 ; Best Local Similarity 20.2%; Pred. No. 0.47;
 ; Matches 145; Conservative 79; Mismatches 251; Indels 242; Gaps 37;
 ;
 ; Qy 25B ARGAAHIAFDENHEGAV-LPDIDITYFCQSSSGTTARGARRDYNSTKPSPEGGER 316
 ; Db 183 AANALKRYDQDGQDLICIPPGVEALERADLAIRPAVIDALLKAMGDASDAAGGSNN 242
 ; Qy 317 ---RLAS --IMADTAHLAHEVIFNTGYEEPTDIKEWPMFTGMEGTPLRNLALGS 367
 ; Db 243 WAWAPRGRATERPILLADPHRVEI--PENYAQHLLACDRDFM-IGL-TVP---- 289
 ; Qy 368 YTARVAGVIGANVFSNSA-----LYTLEVEDSGMT----- 399
 ; Db 290 -----GVPGFPFHFAINGKVAYCVCVTHAFMDTIDLVLEQFAEDGTRARFGNEFEPYAWRRD 343
 ; Qy 400 --AKDGFQGPSPSNRFQFAGPHLAAMPQTODRGHVSQSSTGSNTFEFSYDYLALICGFF 457
 ; Db 344 RIAVRGGADREDIVETRHGPVIAGDP--LEGALITRSYOFAEFLSFCQLTRMP--G 398
 ; Qy 458 APILLARLFYLERCDAAGFTG-GH---GDALKVYTGTDFSEIPOSCLCBHRTRPVCAHT 511
 ; Db 399 ASTVQY-----DATRGWGLIDRNIVAGVNGASLGHLKARVUSPREPENGWLPGWS 452
 ; Qy 512 TYHLR-----ORMPRFGQATROPICVGFGTMNSQY-----SDCDPLGNAYAP--- 553
 ; Db 453 GEHEWWRTPHAMPAR--VTDPPGGLIVTANNRVAHHDPDYLCTDCHP----PYRAE 504
 ; Qy 554 ---LILRKPGDQTEAKATHDT---YRATLRLIFI-DIICERL----- 590
 ; Db 505 RIMERLIVASPAFVDDAAIHADTLSSHVGHLRARLGIQCSLPPEELROTLLIWDGR 564
 ; Qy 591 LDORGAPCSSEGGSVIVDHPFRILDTLARIEQTTFQFMKVVLVETRDYKIREGLSEA- 649
 ; Db 565 MDAGSQARSA-----YNAFRL-----TRLYTARSQHQA 596
 ; Qy 650 THSMALT---FDPYSGAFCPITNFLVRTHLIAVQ---DIALSOCICVFGQOVEGRNF 702
 ; Db 597 AHPPAAVPPGVSPQQGQVWAVPT-LIANDDAGMLKGMSWDELSSEALSV-ATQNLTGRW 654
 ; Qy 703 RNQFQVYERRFYDLENGGETISTRITVTLSEGPSVSP-----NPTLGODAP 749
 ; Db 655 GEBIRP---REFTHPLAQOFPAWAALL---NPVSPPIGGDGTIVANGLVPSSAGEBAT 705
 ; Qy 750 AGRTFDGDLIARVSVEVTDIYKNRVYFS-GNCNTNLSEARARLYGLASAYQRQEKVDM 808
 ; Db 706 YG-----ALSRYTFDVGHDWN-----SRWVV 726
 ; Qy 809 LHGLGFLLKQPHGLLPRGMPPNSKSBNPQW---FWTLLQRNQMPADKLTHEEI 860
 ; Db 727 FHGASG-----HPASHYADQNAAPNSDCANVPMLYSWDRRAAEAVTSQEL 771
 ;
 ; RESULT 16
 ; US-08-541-780-7
 ; Sequence 7, Application US/08541780
 ; Patent No. 5935331
 ; GENERAL INFORMATION:
 ; APPLICANT: Quax, Wilhelmus J.
 ; APPLICANT: Misset, Onno
 ; APPLICANT: Van der Laan, Jan M.
 ; APPLICANT: Lenting, Herman B.M.
 ; TITLE OF INVENTION: Mutated beta-lactam acylase genes
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
 ; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94041
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.26 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/731,157A
 ; FILING DATE: 19910509
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 90200962
 ; FILING DATE: 18 APR 1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER PH.D., BARBARA
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: GBRO-027/000US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-494-7622
 ; TELEFAX: 415-557-0663
 ; TELEX: 380816 COOLBE PA
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 774 amino acids

1 CORRESPONDENCE ADDRESS:
 1 ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
 1 STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
 1 CITY: PALO ALTO
 1 STATE: CALIFORNIA
 1 COUNTRY: USA
 1 ZIP: 94306

1 COMPUTER READABLE FORM:
 1 MEDIUM TYPE: Floppy disk
 1 COMPUTER: IBM PC compatible
 1 OPERATING SYSTEM: PC-DOS/MS-DOS
 1 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

1 CURRENT APPLICATION DATA:
 1 APPLICATION NUMBER: US/08/541,780
 1 FILING DATE:
 1 CLASSIFICATION: 435
 1 PRIOR APPLICATION DATA:
 1 APPLICATION NUMBER: US/07/731,157
 1 FILING DATE:
 1 ATTORNEY/AGENT INFORMATION:
 1 NAME: RAE VENTER PH.D., BARBARA
 1 REGISTRATION NUMBER: 32,750

1 TELECOMMUNICATION INFORMATION:
 1 TELEPHONE: 415-494-1622
 1 TELEFAX: 415-857-0663
 1 TELEX: 380816 COOLEY PA

1 INFORMATION FOR SEQ ID NO: 7:
 1 SEQUENCE CHARACTERISTICS:
 1 LENGTH: 774 amino acids
 1 TYPE: amino acid
 1 TOPOLOGY: linear
 1 MOLECULE TYPE: protein
 1 HYPOTHETICAL: NO
 1 ORGANISM: Pseudomonas species
 1 STRAIN: SEB3

1 US-08-541-780-7

1 Query Match 1.7% Score 106; DB 2; Length 774;
 1 Best Local Similarity 20.2%; Pred. No. 0, 47; Mismatches 21; Indels 212; Gaps 37;
 1 Matches 145; Conservative 79; Mismatches 21; Indels 212; Gaps 37;

Qy 258 ARGAAHLADEFNEGAV-LPPDITYFOSSSGTTARGARRNDYNSTKSPSGGFER 316
 Db 183 AAANALKRYDDGGDLCLCPPGEAERLEADLAALRDAVDALLKANGDASDAAGGSNN 242

Qy 317 -----RLS---IMAADITLALDEVINTGIVYBTPDIKEWPKMFIGMEGTPLRMALGS 367
 Db 243 WAWAPGRPTITGRPLLAGDPHRVEI---PGMYAQHHLACDRDM-1GL-TVP----- 289

Qy 368 YTARVAGTYGAMYFSPNSA-----LYLTTEVEDSGMTE----- 399
 Db 290 -----GVEGPFPFAHNGKVAYCVTHAMDIDYLQFAEDORTARFGNFEFPYAWRD 343

Qy 400 --AKDGGPPSPNRFYQGPAPHAAANPOTDRGHVLSQSQTGSTSYDYLALICGFG 457
 Db 344 RIAVRGGADREFDIVETRGPVIAGDP--LEGAALTLSRSQPAETLSFDOLTRNP--G 398

Qy 458 APILLARLFLYLERCDAGATG-GH-----GDALKYVGTSEKTRPICAHT 511
 Db 399 ASTVAPLY----DATRWGLIDHNLVYAGDVAGSIGHLVRARVSPRENSWLPYGWS 452

Qy 512 TVHLRL---QRMPFRGGATROPIGVFGTMNSQY-----SDCDPLGNYAPY-- 553
 Db 453 GEHWWRGNWPHAMPR--VIDPFGGLVITANNRVVADHPDYLTCHP----PYRAE 504

Qy 554 ---LILRXPQDQEAAKMTDT----XATLRLIFI--DLEQRL----- 590

Db 505 RIMERLVAASPAAVDDAAIAHADTLSPHVGLLARLRLGIQSSLPAELRQLIAMDGR 564

1 Query Match 1.7% Score 105.5; DB 4; Length 1095;
 1 Qy 591 LDRCAPCSSEGSSVIVDHPTRRILDTLRARIEQTTOQMVKVLERDYKIREGLSEA- 649
 1 Db 565 MDASQAAA-----YNAFRAAI 596
 1 Qy 650 THSMALT---FDPSGAFCPTINFLVKRTHLAVQ---DLAISQCHCFYGOQVEGFNF 702
 1 Db 597 AHPPAAVPQGVSPQGQWTAVPTLLRNDDAGMLKGNSWDEALSEALSV-ATCNLTGRW 654
 1 Qy 703 RNOQPVLRFFRPFYDLENGFPISTRSITVTLSGPVSAP-----NPTLGQDAP 749
 1 Db 655 GBEHP---RFTHPLSAQPPAAALL---NPVSRPIGGDGTVLANGLYPSAGFBAT 705
 1 Db 750 AGRTFDDGDLARVSVENTDIRVGNRVS-GNCTNLSSPAAARLVGLASAYORQEKRYDM 808
 1 Qy 706 YG-----ALSRYVTDVGNDN-----SRWVV 726
 1 Db 809 LHGALGFLIKQFHGLFPRGMPNPKSNPQN-----FWTLLQRNOMEPADKLTHEEI 860
 1 Qy 727 FHGASG-----HPASPHYADONAPNSDCAAVPMLYSWDRFAAEAVTSQEL 771

1 RESULT 17
 1 US-09-107-532A-3855 ; Sequence 3855, Application US/09107532A
 1 ; Patent No. 6583275
 1 ; GENERAL INFORMATION:
 1 ; APPLICANT, Lynn A Doucette-Stamm and David Bush
 1 ; TITLE OF INVENTION: AMINO ACID SEQUENCES RELATING TO
 1 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 1 ; NUMBER OF SEQUENCES: 7310
 1 ; CORRESPONDENCE ADDRESS:
 1 ; ADDRESS: GENOME THERAPEUTICS CORPORATION
 1 ; STREET: 100 Beaver Street
 1 ; CITY: Waltham
 1 ; STATE: Massachusetts
 1 ; COUNTRY: USA
 1 ; ZIP: 02454
 1 ; COMPUTER READABLE FORM:
 1 ; MEDIUM TYPE: CD/ROM ISO9660
 1 ; COMPUTER: PC
 1 ; OPERATING SYSTEM: <Unknown>
 1 ; SOFTWARE: ASCII
 1 ; CURRENT APPLICATION DATA:
 1 ; APPLICATION NUMBER: US/09/107,532A
 1 ; FILING DATE: 30-Jun-1998
 1 ; PRIOR APPLICATION DATA:
 1 ; APPLICATION NUMBER: 60/085,598
 1 ; FILING DATE: 14 May 1998
 1 ; APPLICATION NUMBER: 60/051571
 1 ; FILING DATE: July 2, 1997
 1 ; ATTORNEY/AGENT INFORMATION:
 1 ; NAME: Arinello, Pamela Denice
 1 ; REGISTRATION NUMBER: 40,489
 1 ; REFERENCE/DOCKET NUMBER: GTC-012
 1 ; TELECOMMUNICATION INFORMATION:
 1 ; TELEPHONE: (781) 893-5007
 1 ; TELEFAX: (781) 893-8277
 1 ; INFORMATION FOR SEQ ID NO: 3855:
 1 ; SEQUENCE CHARACTERISTICS:
 1 ; LENGTH: 1095 amino acids
 1 ; TYPE: amino acid
 1 ; TOPOLOGY: linear
 1 ; MOLECULE TYPE: protein
 1 ; HYPOTHETICAL: YES
 1 ; ORIGINAL SOURCE:
 1 ; FEATURE:
 1 ; NAME/KEY: misc_feature
 1 ; LOCATION: (B) LOCATION 1..1095
 1 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3855:
 1 ; US-09-107-532A-3855

Best Local Similarity 18.9%; Pred. No. 1; Matches 145; Conservative 112; Mismatches 298; Indels 211; Gaps 35;

Qy 551 APYLIRKPGDQEAAKATMODYTATRLRFLIDLEQERLDRGAPCSEGLS-----S 604
Db 360 APTDTPPTTTIKAGETIYTTSKNAEQKGQILDKSG-VEGSDLWNTSLAGNTFA 418

Qy 605 VIVDHPTFRRIID-TURARIQBTTOFMRKVLTVERDYKIREGLSEATHSMALTFDP---- 659
Db 419 IRKDPTGEVQEMTIDENHAEATPREIANALEGTYVTE--TRASIGFVNTEKFVKVE 476

Qy 660 -YSGAFCPCTPNLVKRTHLAVQDLS-----SOCHCYFYGGOV-----EGR- 700
Db 477 LKYANQTVLAVTSNTYKQGKRAQKRAVFGTETYLTAKDKA 536

Qy 701 -NFRNQFQPVLRRPFYDLFNGFPISTRSTVTLSEGPVSP----NPTLGQD-APAGR 752
Db 537 VKWSAFKP-----EMYGTKADETWTALDEKNGQAKHLAINYYWQSTKAPGY 589

Qy 753 TFDGDILARVSE-----VIRDIRYTNRVV-----FEGNCNTNLSEA----- 788
Db 590 TLDETKPVSIKKVDDNEKNIAVITRDVTAXEQITRGFDFFEKAGSAAGTAETGENDLTF 649

Qy 789 -RARLUGLASAYORQEKRVTMLHGALGF-----LJKQFPHGLFPRGM---- 829
Db 650 KVSPLEGTNBTTGADEATPAYNEOLGFDYGYKFLBEVEA-----BEGFQKIT 706

Qy 830 PPNKSKP-----NPQFWTLLQRNQ-----MPADKLTHEETTIAAVKRFTREE 872
Db 707 PLEIRSTFKENKEDFVKSEYVFITEQDKQPKIKIVTVPYEXLTN-----KAFSVS 757

Qy 873 YAATINFNLD--PTCIGELAQFYWMANLIRKCDHSQYLINTLTSITGARRPRDPSSVLU 930
Db 758 INRLMYLDPEEDSUTSLATWKCGNKELTSLSDE-LVDKL-----SYNLH 803

Qy 931 WIRKD--VTSAADIETOAKALLEKTELENBLWTAFTAFTSHLYRAAMN---QRPMV-- 980
Db 804 EIKEDYVVAQDIDYA-TKAAQEDKAKPV-VIAETATLANKETGTWKQHKTAE 861

Qy 981 -VLGISISKYHGAAGNRNRVOAGHNWGLNGKNYCPLFFDRTRFLIACPRGGFICPVT 1039
Db 862 QVLNKTIVLNNVYENKEAPEGD-----KPEVA 889

Qy 1040 GPSSGNRETLSDQVRGIIYTGAMVQLAIYATVYRAGARAQMAFDWLTSUTDDELA 1099
Db 890 -----KDVSLANNOQTVSTCVERHVSICONTKAHLENG---SQFTFHGDVMDFFDVSI 939

Qy 1100 RDL---BEDDQIQTQLETPWTEGALEVKILDE-----KTT-----AGDGETPML 1144
Db 940 HDVLDGSKEAFTIYLALLPDGTKEIWKGKIEVNDKEFTKTVLAKKVDTGKYPGT 999

Qy 1145 AFNFDSCEPSHDITSN----VLNISGSNSISGSTVPGLKRPEDDE 1185
Db 1000 KFTFABINYDKDGTINGKNERNEDLKBSQTJTPKEVPTILSTPKOPE 1045

Qy 413 YQFAGPHIAANPQDTRGCHVLSQSOSTSNTSFSDYLAICFGAFLPILLFYLERCD 472
Db 359 ETRHGPVIAGDP---RGAAULTLRSVQFAETDLSFDLTRLNP-GASTVQALY----D 407

Qy 473 AGAFTG-GH---GDALKYKTGTDESEIPSLCERTRPYCAHTTVMHRLR-----ORMP 521
Db 408 ATRGWGLIDHNTIVAGDVAGS1GHLYRVRSPRENGWLPWGWSGEHENGWIPHEAMP 467

Qy 522 RFQOATQPIGVFGTNISQY-----SDCDPLGNYAP-----LILRKPCGDQTE 564
Db 468 R---VLDPPGG1TIVTANTRVYADDHPDYLCDCHP---PYRAERIMKRLIVANPAFAVD 519

Qy 565 AKATMODYTATRLRFLIDLEQERLDRG-PCSSBGLSSTV-----D 608
Db 520 DAAIATHDLSP---HVGLLRRRLALGARDSSAEGLRQMLVAWGRMDAASEVASA 574

Qy 609 HPTFRRIIDLT---RARIQETTQ-----FMKVILVETRDYKIREG--- 645

STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/633,760
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-929-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-1000
TELEFAX: (703) 413-2200
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US -08-633-760-46

Query Match 1.7%; Score 105; DB 1; Length 74;
Best Local Similarity 20.7%; Pred. No. 0.6;
Matches 146; Conservative 76; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--AGAACARERFGRFGRSRCQQGPPVDAVETTGAB-ICTR---LGLBEPNTILYLVTTAL 161
Db 70 LTRRKAGLGRAAWLGL--AEAEEADIIVRLRGMKEMYKQRDPEALGYEAKD-----M 117

Qy 162 FKEAVFMCNVFLHYGGDIVHINHGDVTRIPLEFPVOLFMPDVNRLYDPFPNTTH---R 216
Db 118 LRAYVAGYNAFLASGA-----PL-PVEYGLGAE---PEPWPHWSTAVMR 159

Qy 217 SIEGFYFPTPPYNTGICHLLHDCTVAPMAYALRVNTAV---ARGAAHLAFDENHEG 272
Db 160 RIG-----LIMGAVWFKLWMLALPVVGZANALKRYDODGRD 197

Qy 273 AV-LPPDITYTYFQSSSGTTTARGARNDYNSTSXPSPSGFFER----RLAS---IM 322
Db 198 LLCLIPPERGAEADRLEADLTLRPAVDALLKAYGDDA-DAAGGGSNNWAVAPERTATGRPIL 257

Qy 323 ADTALHAEVINTG3YBETPTDIKMPMFQMGETLIPRNALGSYTARVAGVGMVFS 382
Db 258 AGDPHRYFBI---PGMVAQHILACDNEFM-IGL-TVPP-----GVPGFPHFA 298

Qy 383 PNSA-----LYTEVEDGMTE-----AKOGPGPBPNRF 412
Db 299 HNGKVAICVTHAFMDIDYLQEPAFGEGRTARFGNDFFEPYAWSRDRIAVRGGADREFDIV 358

Qy 413 YQFAGPHIAANPQDTRGCHVLSQSOSTSNTSFSDYLAICFGAFLPILLFYLERCD 472
Db 359 ETRHGPVIAGDP---RGAAULTLRSVQFAETDLSFDLTRLNP-GASTVQALY----D 407

Qy 473 AGAFTG-GH---GDALKYKTGTDESEIPSLCERTRPYCAHTTVMHRLR-----ORMP 521
Db 408 ATRGWGLIDHNTIVAGDVAGS1GHLYRVRSPRENGWLPWGWSGEHENGWIPHEAMP 467

Qy 522 RFQOATQPIGVFGTNISQY-----SDCDPLGNYAP-----LILRKPCGDQTE 564
Db 468 R---VLDPPGG1TIVTANTRVYADDHPDYLCDCHP---PYRAERIMKRLIVANPAFAVD 519

Qy 565 AKATMODYTATRLRFLIDLEQERLDRG-PCSSBGLSSTV-----D 608
Db 520 DAAIATHDLSP---HVGLLRRRLALGARDSSAEGLRQMLVAWGRMDAASEVASA 574

Qy 609 HPTFRRIIDLT---RARIQETTQ-----FMKVILVETRDYKIREG--- 645

GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: FUJIMURA, TAKAO
APPLICANT: ISHII, YOSHINORI
APPLICANT: NOGUCHI, YUJI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK,
P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON

RESULTS 19
 US-08-633-760-48
 ; Sequence 48, Application US/08633760
 ; Patent No. 5804429
 GENERAL INFORMATION:
 APPLICANT: NIWA, MINBO
 APPLICANT: SAITO, YOSHIMASA
 APPLICANT: FUJIMURA, TAKAO
 APPLICANT: ISHII, YOSHINORI
 APPLICANT: NOGUCHI, YUJI
 TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESS: P.C.
 STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ALEXANDRIA
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22222
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/633,760
 FILING DATE: 01-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 18-929-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 774 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-633-760-48

Query Match 146: Conservative 1.7%; Score 105; DB 1; Length 774;
 Best Local Similarity 20.7%; Pred. No. 0..6; Mismatches 241; Indels 37;

Matches 109 LTR-ACNAARERGFSRCQGPVVDGAVETGAE-ICTR--LGHEPENTILYLVTTAL 161
 Db 70 LTARKALGRAEING--AEEAADILVRLGRMEVKRRDFALGYBAKD-----M 117

Qy 162 FCGAVEMCNVFLHYGLDIDVHNGDVTRIPLFVQLFMPDYNRLVPDPATHH---R 216
 Db 118 LRAYVAGTNAFLASGA-----PL-PVEYGLGAE--PEPWPHSTAVMR 159

Qy 217 SIGEGFYYTPFPYNTGLCHLHDVCVIAFMAYALRVNVTAV---ARGAHLAFDENHEG 272
 Db 160 RLG-----LNGSVWFLKWMALIFVGANAKLARYDDGGRD 197

Qy 273 AV-LPPDITYTYFQSSSGTTARGARRNDVNSTSKEPSGCFER----RLAS--IM 322

Db 198 LICPPGAEADRDEADLRLPAVDALLKAMGGDASDAAGGSNNWAVAPGRTAIGRPL 257

RESULTS 20
 US-08-931-608A-5
 ; Sequence 5, Application US/08931608A
 ; Patent No. 6302685
 GENERAL INFORMATION:
 APPLICANT: Lobel, Peter E.
 APPLICANT: Sleat, David E.
 TITLE OF INVENTION: NOVEL HUMAN LYOSOMAL PROTEIN AND METHODS OF ITS USE
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,608A
 FILING DATE: 01-JULY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson, Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 601-1-077
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 635 amino acids
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO

US-08-931-608A-5

Query Match 1.7%; Score 104.5; DB 4; Length 635;
Best Local Similarity 21.0%; Pred. No. 0.47; Gaps 14;
Matches 77; Conservative 36; Mismatches 121; Indels 133; Gaps 14;

Qy 245 MAVALRVRNVTAVRGAAHLAFAFDENH-EGAVLPDIDITYFQSSSGCTTARGARRNDVN 303
Db 10 VAIAMLAMSSLAHED---AWSTHTQAMSPPASTOVLAASTSATTTGNA--YTLN 62

Qy 304 STSKPSPGFERLALASIMAADTLHAEVNTGIVYBTPDIKEWMFIGMEGTIPRLN 363
Db 63 MTGSPRIDEA---AVTALEADPILHEVALK-----DRNPD 95

Qy 364 ALGSYTYARVGIGAMVPSNSALYLTEVEDSGMTAEKDGGCGPSFNRFYQAGPHILAAN 423
Db 96 ALOFLAGYT----TGSALFGKPLTPSQTET----RF----GP----127

Qy 424 PQTDRGHVVLSQQTGSNTTEFSVDYLALLIGCPAPLIARLLFYLERCDAGAFTGGHDDA 483
Db 128 TQSQVDAVVAHLQAOAGFINEVPNRL-LISADGT----AGAATNGFRTS 172

Qy 484 LKYVGTGFDFSEIPCSLCXTRPVCAHTTVHLRQRMRMFRQQATRQPPIGVFTMNQSD 543
Db 173 IK-----RFSANGR-----181

Qy 544 CDPLGNAYAPYLILRKPGDQEAAKATMDTYRATLERLFDIQLDGRAPCSSEGSL 603
Db 182 -EFFANDAPALVPSLGDGSNAVGLQNYSVKHTLHHVY--HPEDVTVGPNVGTOAAA 237

Qy 604 SVTIDHP 610
Db 238 AVAAHHP 244

RESULT 21
US-09-851-847-5
Sequence 5, Application US/09851847
Patent No. 6638712
GENERAL INFORMATION:
APPLICANT: Lohel, Peter
Sielert, David E.

TITLE OF INVENTION: NOVEL HUMAN LYPOSOMAL PROTEIN AND METHODS OF ITS USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,847
FILING DATE: 09-May-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/931,608
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, Esq., David A.

REGISTRATION NUMBER: 26,742
REFERENCE DOCKET NUMBER: 601-1-077
TELECOMMUNICATION INFORMATION:
PHONE: 011-7-5800
TELEFAX: 201-43-1684

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 635 amino acids
TYPE: amino acid
STRANDBNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-851-847-5

Query Match 1.7%; Score 104.5; DB 4; Length 635;
Best Local Similarity 21.0%; Pred. No. 0.47; Gaps 14;
Matches 77; Conservative 36; Mismatches 121; Indels 133; Gaps 14;

Qy 245 MAVALRVRNVTAVRGAAHLAFAFDENH-EGAVLPDIDITYFQSSSGCTTARGARRNDVN 303
Db 10 VAIAMLAMSSLAHED---AWSTHTQAMSPPASTOVLAASTSATTTGNA--YTLN 62

Qy 304 STSKPSPGFERLALASIMAADTLHAEVNTGIVYBTPDIKEWMFIGMEGTIPRLN 363
Db 63 MTGSPRIDEA---AVTALEADPILHEVALK-----DRNPD 95

Qy 364 ALGSYTYARVGIGAMVPSNSALYLTEVEDSGMTAEKDGGCGPSFNRFYQAGPHILAAN 423
Db 96 ALOFLAGYT----TGSALFGKPLTPSQTET----RF----GP----127

Qy 424 PQTDRGHVVLSQQTGSNTTEFSVDYLALLIGCPAPLIARLLFYLERCDAGAFTGGHDDA 483
Db 128 TQSQVDAVVAHLQAOAGFINEVPNRL-LISADGT----AGAATNGFRTS 172

Qy 484 LKYVGTGFDFSEIPCSLCXTRPVCAHTTVHLRQRMRMFRQQATRQPPIGVFTMNQSD 543
Db 173 IK-----RFSANGR-----181

Qy 544 CDPLGNAYAPYLILRKPGDQEAAKATMDTYRATLERLFDIQLDGRAPCSSEGSL 603
Db 182 -EFFANDAPALVPSLGDGSNAVGLQNYSVKHTLHHVY--HPEDVTVGPNVGTOAAA 237

RESULT 22
US-08-019-870-5
Sequence 5, Application US/08019870
Patent No. 5336613
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: YOSHIMASA, SAITO
APPLICANT: SASAKI, HITOHI
APPLICANT: ISHII, YOSHINORI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
CITY: Washington D.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/019,870
FILING DATE: 1993-02-19
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, No. 5336613man F.
REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 18-791-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 248855 OPAT UR
 SEQUENCE CHARACTERISTICS:
 LENGTH: 774 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-019-870-5

Query Match 1.7%; Score 104.5; DB 1; Length 774;

Best Local Similarity 21.7%; Prod. No. 0.68;
 Matches 91; Conservative 41; Mismatches 136; Gaps 19;

Qy 372 VAGVIGAMWFSPPNSA-----LYITVEDOSGMTE-----AK 401

Db 288 VPGPGFPFAHNGKVACVTHAFMDIHDLYLEPAGEGRTARFGNDPEPYAWSRDRIAV 347

Qy 402 DGGPGPSFTRFYQFAGPHLAANPOTDRGHVLISSQSTSCTSSNTESVYLA-----LI 453

Db 348 RGGADEFREFFIVETPHGPVAGDP--RIGAALTLSRVSQFAETDLSFDCLTRMPGASHNLV 404

Qy 454 CGEGAPLLFLYLERCDAGAFTGGHGDALKYVGTGFD--SEIPCSLCEKTRPVCAHT 512

Db 405 AGDVAGSIGHLVTVQLYDA---TRG-----WGLIDRARVPSRDRENGMLPVPGWSG 453

Qy 513 VHRRL---QRMRFRGQDTROPIGVFGTMNSQY-----SPCDPLGNYAPY--- 553

Db 454 EHEVRGWIHPMEAR---VTDPPGCIIVTANNRVAADDHPDYLCTDCHP----PRAER 505

Db 554 ---LILRKQDGQTEAAKATMQDTYRATERLFLDQEQLRDLRGAA--PCSSBGLSSVV- 607

Qy 506 IMKRVIANFAAVDDAAAHADTLSP----HYGLLRRLEAIGARDSSAAGLROMLVA 560

Qy 608 -----DHPTRFLDLT---FARIEOTTQ-----FMKVL 634

Db 561 WDGRMDAASEVASYASNAFRAALRPLVTDQSGLQAIISHPEAAVPGVSPQQVWWAWAFTP 620

Qy 635 VETRYKIREG-----LSEA-----THSMWLTDFDSGACCP 666

Db 621 LRDDDAAGMLKGWSWDQALSEALSVAQNLTGRSMGEERPRFTPLATOFPAWAGLNP 679

RESULT 23
 US-08-811-519-1

i Sequence 1, Application US/08811519B

i Patient No. 663035

i GENERAL INFORMATION:

i APPLICANT: Petrenko, Alexandre

i TITLE OF INVENTION: CALCIUM INDEPENDENT RECEPTOR OF ALPHA-LATROTOXIN,

i FILE REFERENCE: 1049-1-007

i CURRENT APPLICATION NUMBER: US/08/811,519B

i NUMBER OF SEQ ID NOS: 31

i SOFTWARE: PatentIn Ver. 2.0

i SEQ ID NO: 1

i LENGTH: 1471

i TYPE: PR

i ORGANISM: rat

i US-08-811-519-1

Query Match 1.7%; Score 104.5; DB 4; Length 1471;

Best Local Similarity 19.6%; Prod. No. 2.3; Mismatches 98; Indels 339; Gaps 47;

Matches 182; Conservative 98; Mismatches 310; Indels 339; Gaps 47;

Qy 73 LAGAGITLKLTSTSHFYPSPVVFHGGKHLSSAAAPNLTRACNAAERFRFSR---CQGP 128

Db 4 LAAABMSLCVTT-----VIVTASATGSLR---AGLPGSMRRELACEY 44

RESULT 24

US-08-019-870-3

; Sequence 3, Application US/08019870

; General Information:

i APPLICANT: NIWA, MINEO

i APPLICANT: YOSHIMASA, SAITO

i APPLICANT: SASAKI, HITOSHI

i APPLICANT: ISHII, YOSHINORI

i TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE

i NUMBER OF SEQUENCES: 42

i CORRESPONDENCE ADDRESS:

Qy 129 PVDGAVETTGAEICTRGLPLENTILYLVVTALKEAVFCMCNVFLHYGGLDIVHI---NH 185
 Db 45 PIE-----LRCGSDYIMVEANY 63

Qy 186 G-----DVTIRPLPFIQOLMFDVNLLVPDPNTNHSI---GEGFVYPFBRYNTGLC 234
 Db 64 GRTDKKICDADPFPMENTQCYLPFAKLMQSQRNCRNTQVVVAGSDAEPDPGTYKYL- 122

Qy 235 HLIBDCVIAPMAVALVRNNTAVARGAHLAFD---ENFEGA-----V 274

Qy 123 EVQDC-----VPIVKEQKVFCPGTLQKLEPTTHESEHOSGACKDPLQAGDRIVY 176

Db 275 LP--PDITYTQFQSS-----SGTATTGARRNDVASTSKSPSGF-----E 315

Db 177 MPWIXRTDILTEVASWEDYVAARHTTYRLPNRD-----GTFVYYDGAVFYNK 227

Qy 316 RRLASIMAADTALH--AEVIFTNTGYEET-----PTDIK-----EWPMFTGMEGT 358

Db 228 ERTRNWKVLDLRTRISGETVINTANYHDTSPIEWGGKTIDLAVIDENGWLWVY-ATIGN 286

Qy 359 LPRL--NALGSYTAVARAG-----VIGAMVFSSENSALYLTVEYED 394

Db 287 NGRLIVSQNPYNTURFEGTWETGYDKRSASNAFMVCGVLYLVRSEVYDDDEAAGNRVYD 346

Qy 395 SGMTBKDGPF-----GPSFNRFY-----QFAGPHLAAHQ 425

Db 347 AFNTNAANREPVSIAFPNPYQFVSSVDPNRPDNQLYWNNYFVYRYSLEFGPPDPSAGEA 406

Db 426 TDRGTVLSSQGSTGSNTESVYDYLALIICF-GAPLILARLLFYLERCDAGAFTGHDGL 484

Qy 407 TSPP--LSTTTTARPPLTSTAATTPLRRAPLITPGVAGAINL-----GPDL 454

Qy 485 KXVGTGFDSPELPCSLCEKTRP--VCAHTTVHLRQRMRFRGOATRQP----- 530

Db 455 PPATAFAPSTRPRAFPNLYHSPELCFPREVRVYQPATQQGMLVYRCPKGTRGIASFQ 514

Qy 531 ---IGVFGTMNSQSYDC-DPLGNYAPYLJLRKPGDQ----TEBAKATMQDTYRATLBR 580

Db 515 CLPALEGWNPRGPDLISNCTSREWNOVAQKI--KSENNAANTIASLARHT----- 561

Qy 581 LPIDLEQERLLDRAFCSSGLSSVYDHTPFRRLDTIPIARI----- 623

Db 562 -----RGSTYAGDQVSSS---KLMEQDILIDQAQLQRLRPIERESAGKNYNK 605

Qy 624 ---EQTTOQMVKLVETRDYKIR-EGL-----SEATHSMALTEDPY-SGACPITN 669

Db 606 MHKRERTCKDQYIKAVETVNDLRLPAALESWQDNATEQVHTATMLDVLEGAFLADN 665

Qy 670 -----FLVGRTHLAV-----VODIALSOCHCVFVGQVQVBGRNFR-NQFOPVLR 712

Db 666 VREPARPLAAQNVVILETVISTEGGVQELVFPQBYAESSESSIONSANTIKONSRNQVVKV 725

Qy 713 RFVDFLIPN--GGF1STRSITYVTL---SEGVSAPNPLSQ-----DAPAGRTPDGLA 759

Db 726 VPI-LMNNGLFSLSTENATVKGZGTGGPGGASUVNSQVIASSINKESSRVP--LM 781

Qy 760 RVSVETVIRDYKVNRYVFSGNCT--NLSE 786

Db 782 DPVIFTVAHLERKH--FNANCFSWNTSE 808

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESS: P.C.
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICANT: US/08/019,870
 FILING DATE: 19930219
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 531661 man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 18-791-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEX: 243855 OPAT UR
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 774 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-019-870-3

Query Match 1.6%; Score 103; DB 1; Length 774;
 Best Local Similarity 20.5%; Pred. No. 0.97;
 Matches 143; Conservative 80; Mismatches 248; Indels 226; Gaps 37;

Qy 109 LTR--ACNEARERGFSRCCGPPYDGVETTGAE--ICTR---LGLEPENTILLYVVTAL 161
 Db 70 LTRKALGRAAEWLG--AEEAADILYRLIGMEKVCRDPEALGVEKD----M 117
 Qy 162 FKEAVFMCMVFLHYGGLDIVTHNGDVIRPLFVQLMPMDYARLPDPFTNTH----R 216
 Db 118 LRAYTAGVNIFLASCAS----PL-FEVYGLGAE--PDPWEPHSINMR 159
 Qy 217 SIGEGFVYPFPYNTGLCHIJDCVIAPMAVALRVNNTAV----ARGAHAFLDENHEG 272
 Db 160 RLG-----LLMSWFLWMLALPVGAANALKRYDDGGRD 197
 Qy 273 AV-LPFDITTYQSSSGTTTARGARNDVNTSKSPSNSGER----PLAS---IM 322
 Db 198 LLCPPGAERDRLEDLATURPAVDALLKMGCGDASDAAGGGNNWAVGPTATGPIL 257
 Qy 323 AADTLHAEVTFNTSUYEETPTDIKEWPMPFIMGEGTLPLNALGSYTARVAGVIGANVFS 382
 Db 258 AGDPRHRVET--POMYAQHHLACDRDM-IGL-TVPGPFPHAH----GKAYS 306
 Qy 383 PNSA----LYLTPEVEDSGNTE----AKDGGPGPSFNRFYQFAGHL 420
 Db 307 VTHAPMDIHDLYLEOFGABERTARFGRNDTEPVAMSRSRDAVRGCADEFIDVTRHGPVI 366
 Qy 421 RANPQTDRGIVLSSQSTGSSNTESVYDYLALICGFGAPILLAFYLERCDAGAFTG-- 478
 Db 367 AGDP--RDGAALTURSVQAEETDLSFDCLTRMP--GASTVAQLY----DTTRGHLI 415
 Qy 479 GH---GDAKXYVTGTDFSEIPCSLCXKHTRPVCAHTTHTRL---QRMPPREGQATRQ 529
 Db 416 DHNLVAGDVASGHILVRAVSPSRPRENGLPVPGWSGHWRGWIPEAMPR--VTDP 472
 Qy 530 PIGVFCTMNSY----SDCDPLGNYAPY----LIRRKPGDQEAKATMQD 572
 Db 473 PGIIIVTANNRVVADDHPDYLTCDHP----PYRAERIMKRVLVANPAVDDAAATHAD 527
 Qy 573 TYRATLRLFIDLEOERLIDRGA - PCSSIEGLSSVIV----DHFPTFRRL 616

RESULT 25
 US-08-633-760-44
 / Sequence 44, Application US/08633760
 / Patent No. 5804429
 / GENERAL INFORMATION:
 / APPLICANT: NIWA, MINEO
 / APPLICANT: SAITO, YOSHIMASA
 / APPLICANT: FUJIMURA, TAKAO
 / APPLICANT: ISHII, YOSHINORI
 / APPLICANT: NOGUCHI, YUJI
 / TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
 / NUMBER OF SEQUENCES: 64
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 / ADDRESSEE: P.C.
 / STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
 / CITY: ARLINGTON
 / STATE: VIRGINIA
 / COUNTRY: USA
 / ZIP: 22202
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 COMPUTER: PC-DOS/MS-DOS
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/633,760
 FILING DATE: 01-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 18-929-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2200
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 774 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-633-760-44

Query Match 1.6%; Score 103; DB 1; Length 774;
 Best Local Similarity 20.6%; Pred. No. 0.97;
 Matches 145; Conservative 77; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--ACNAARERFGERGERCOCGPVPDGAVENTGAE-ICTR---LGLEPENTILLYVVTAL 161
 Db 70 LTRKALGRAAEWLG--AEEAADILYRLIGMEKVCRDPEALGVEKD----M 117
 Qy 162 FKEAVFMCMVFLHYGGLDIVTHNGDVIRPLFVQLMPMDYARLPDPFTNTH----R 216
 Db 118 LRAYTAGVNIFLASCAS----PL-FEVYGLGAE--PDPWEPHSINMR 159
 Qy 217 SIGEGFVYPFPYNTGLCHIJDCVIAPMAVALRVNNTAV----ARGAHAFLDENHEG 272
 Db 160 RLG-----LLMSWFLWMLALPVGAANALKRYDDGGRD 197
 Qy 273 AV-LPFDITTYQSSSGTTTARGARNDVNTSKSPSNSGER----PLAS---IM 322
 Db 198 LLCPPGAERDRLEDLATURPAVDALLKMGCGDASDAAGGGNNWAVGPTATGPIL 257
 Qy 323 AADTLHAEVTFNTSUYEETPTDIKEWPMPFIMGEGTLPLNALGSYTARVAGVIGANVFS 382
 Db 258 AGDPRHRVET--POMYAQHHLACDRDM-IGL-TVPGPFPHAH----GKAYS 306
 Qy 383 PNSA----LYLTPEVEDSGNTE----AKDGGPGPSFNRFYQFAGHL 420
 Db 307 VTHAPMDIHDLYLEOFGABERTARFGRNDTEPVAMSRSRDAVRGCADEFIDVTRHGPVI 366
 Qy 421 RANPQTDRGIVLSSQSTGSSNTESVYDYLALICGFGAPILLAFYLERCDAGAFTG-- 478
 Db 367 AGDP--RDGAALTURSVQAEETDLSFDCLTRMP--GASTVAQLY----DTTRGHLI 415
 Qy 479 GH---GDAKXYVTGTDFSEIPCSLCXKHTRPVCAHTTHTRL---QRMPPREGQATRQ 529
 Db 416 DHNLVAGDVASGHILVRAVSPSRPRENGLPVPGWSGHWRGWIPEAMPR--VTDP 472
 Qy 530 PIGVFCTMNSY----SDCDPLGNYAPY----LIRRKPGDQEAKATMQD 572
 Db 473 PGIIIVTANNRVVADDHPDYLTCDHP----PYRAERIMKRVLVANPAVDDAAATHAD 527
 Qy 573 TYRATLRLFIDLEOERLIDRGA - PCSSIEGLSSVIV----DHFPTFRRL 616

Query Match 1.6%; Score 103; DB 1; Length 774;
 Best Local Similarity 20.6%; Pred. No. 0.97;
 Matches 145; Conservative 77; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--ACNAARERFGERGERCOCGPVPDGAVENTGAE-ICTR---LGLEPENTILLYVVTAL 161
 Db 70 LTRKALGRAAEWLG--AEEAADILYRLIGMEKVCRDPEALGVEKD----M 117
 Qy 162 FKEAVFMCMVFLHYGGLDIVTHNGDVIRPLFVQLMPMDYARLPDPFTNTH----R 216
 Db 118 LRAYTAGVNIFLASCAS----PL-FEVYGLGAE--PDPWEPHSINMR 159
 Qy 217 SIGEGFVYPFPYNTGLCHIJDCVIAPMAVALRVNNTAV----ARGAHAFLDENHEG 272
 Db 160 RLG-----LLMSWFLWMLALPVGAANALKRYDDGGRD 197

QY 273 AV-LPPDITYTQFQSSSSGTTARGARRNDVNSTSKPSGGFER-----RIAS---IM 322
 Db 198 LLCIPPGRAEDRREADLTLRPAVDALLKANGDASDAAGGSNTNVAPERTATGRPLI 257
 Qy 323 AADTALHDEVIFNTGIVETTPDIKEPMFICMEGTLPRNALGSYTARYAVIGAMVFS 382
 Db 258 AGDPHRVEFI---PGYQAQHHACDRDM-1SU-TVP-----GVPEPFPFA 298
 Qy 383 PNSA-----LYLTIVEDSGME-----AKDGPGSFNR 412
 Db 299 HNGKUAVCYTHAFMDIHDLLEOFGAGCTARFGNDPEPVANSRDRIAVRGGADREFDIV 358
 Qy 413 YQFAGPHUAANPQTDRDGHVLSSTGSSNTFSVDYLALICFGAPLLARLLFYLERCD 472
 Db 359 ETHHGPVTAIGDP---RDEAALTIRSVOFAETDJSFDLTRMP---GASTVQLY---D 407
 Qy 473 AGAFTG---GH---GDALKYTGTEDSEIPCSLCEKHTRPYCAHTTIVHRLR-----QRMP 521
 Db 408 ATRCWGLIDHNLYAGDVAGSIGHLVRSPREPNWLPVQGWGSHENWGWIHEAMP 467
 Qy 522 RFGQATROPPIGVFTGTMQSQY-----SDCDPLGMNAPY-----LLRKPGDQTE 564
 Db 468 R---VIDPFGGIIVTANRVRVADDHPDYLTCDHP---PTRAERIMKLVLVANPAFAVD 519
 Qy 565 AAATMQDTYRATERLFLDQEPLRLLGA--PCSSRGFLSSVIV-----D 608
 Db 520 DAAIIHADLSP----HYGLLARRLEAAGLDSAAEGLRQMLVAWDGRMDAASEVASA 574
 Qy 609 HPTFRILDTL---RARIEQTTO-----FMKVLYVETRDYKIRKG---645
 Db 575 YNAFRRAUTRLVTDTRSLGLQALISHPFFAAVAPGYSQPGQWWVAPTLRDDAGMLKGWSN 634
 Qy 646 ---LSEA-----THSMWALTFDPYSGAFCP 666
 Db 635 DQALESAVSASONLTGRSGWGBEHPRPFTHPLATQFPAWAGLNP 679

RESULT 27
 US-08-070-165F-6
 ; Sequence 6, Application US/08070165F
 ; Patent No. 5750355

; GENERAL INFORMATION:
 ; APPLICANT: Chiu, Ing-Ming
 ; ATTORNEY: Poulin, Matthew L
 ; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ing-Ming Chiu
 ; STREET: S2012 Davis Medical Research Center, 480 West
 ; STREET: 9th Avenue
 ; CITY: Columbus
 ; STATE: Ohio
 ; ZIP: 43210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/070,165F
 ; FILING DATE:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (614) -293-8093
 ; TELEFAX: (614) -293-5611
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 729 amino acids
 ; TOPeLOGY: linear
 ; MOLECULE TYPE: protein

US-08-070-165F-6

Query Match 1.6%; Score 102; DB 1; Length 729;
 Best Local Similarity 20.1%; Pred. No. 1.; Gaps 26;
 Matches 69; Mismatches 206; Indels 168;

Qy 82 LITSHYPSPVFVHGKHTVLEPSSAAPNLTRACHAARERRGFSRCQGPFDGAVETTGAEI 141
 Db 928 LAVGYAEPSSIVF---GRHAPGAGGTFSQIGNATELYG---S1PNPTLDFGTTLTG---981

Qy 142 CTRLGHEPENTILYLVVTLFKEAVEMCNVFLHY----GGDLIVHNGDVRIPLEPV 196
 Db 982 ---AFSADGTVVFLSDGPGRVYPPYSNLPDISSAAAEGFVTVPGVSDI-----1029

Qy 197 QLFMPD-VNRLVPPDENTHRSIGEG-FVYPTPFYNTGLCHLHDCTVAPMAVALVRRNV 254
 Qy 404 GPGSPFNRPFYQFAGPHI-----ANPQTDRDGH-----VLSQSTGSSNTESVDYLAL 452

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NO. 5192678man F.
REGISTRATION NUMBER: 24, 618
REFERENCE/DOCKET NUMBER: 18-709-0
TELEPHONE: (703) 521-4500
TELEFAX: (703) 486-2347
TELEX: 248855 ODAT UR

SEQUENCE CHARACTERISTICS:
LENGTH: 774 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: Protein

US 07-147-90A-3

Query Match 1.6%; Score 102; DB 1; Length 774;
Best Local Similarity 20.6%; Pred. No. 1.2;
Matches 145; Conservative 77; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--ACNAARBERGFSRSGQPPDGAETTGBE--ICTR---LGLEPENTILYLVTTAL 161
Db 70 LTRRKALGRAENLG--AEEAADILYLRLGNEKVERDFEALGVAKD-----M 117
Qy 162 FKEAVFMNVFLHFLYGLDLVHNGDVIRIPLPVQLMPDVNRLVPDPFNTH---R 216
Db 118 LRAVAGNAFLAGA-----PL PVEYGLGAE---PEPWEPHSLAVMR 159
Qy 217 SIGEGFVYPTPFYNTGLCHLIHDCTVAPNALVRVNTAV---ARGAHHIAFDENHEG 272
Db 160 RLG-----LLMGSUWPKLWRMLALPVUGAANALKURDYDDGRD 197
Qy 273 AV-IPPDITYTYFQSSSSCTTARGARRDNVNSTSKPPEQQGFER---RLAS---IM 322
Db 198 LLCPGGAEDRLEADLTLRPAVDALLKAMGDASDAGGGNNNWAVGRTATGRPL 257
Qy 323 AADTAHALHAVIYNTGIVYETPTDIKEWPMPFIGMEGTLPRLNALSYTARVAGVGMVFS 382
Db 258 AGDPHRVFEI---PGMYAQPHLACDRFDN-IGL---TVP-----GVGFPHFA 298
Qy 383 PNSA-----LYLTVEDSGMT-----AKDGGGPSPENRP 412
Db 299 HNGKVAYCITHAFMDIHDDLUQPAGEGTTARFGNDFFBPAVNSRDRTAVGGAADREDDIV 358
Qy 413 YQFASPHLAAANPOTRDGEVFLSSGTSGSTSNTFEDVYLALLCGFAPLALARFLYLERCD 472
Db 359 ETRHGPVIAGDP--RDGAALTLSRVQFETLSDFDCLTRMP--GASTVAGLY----D 407
Qy 473 AGAFTG--GH---GDAKXCVTGTFDSELPCLSCLEKHTRPAVCAHTTVHLR----ORMP 521
Db 408 ATRGGLIDNLVADEVASSIGHLYRARVSRSRPRENGWAVPWCNSGEHWGWHIPAMP 467
Qy 522 RFQGATROPIGVFTMNQY-----SDCDPLGNYAH-----LILRKPGDQTE 564
Db 468 R---VTDPPGSIITVANNYVADDHPDYCTDCHP----PYAERIMKRLVANPAPAVD 519
Qy 565 AAATAHQDTRATLERLFIDQEPLLBDQA--PCSSSGBLSSIV-----D 608
Db 520 DAAAATHADLSP----HYGLLRRRLREALGARDSSAEEGRMLVANDGRMDAASEVASA 574
Qy 609 HPTPRILDT---RARIBETTTQ-----FMKVVLVETDVKIREG---645
Db 575 YNAPRPAALTIVTPSGLIEAISHPPAAYARGVSPQGQWWAVPTLRLDDAGMLKGNSW 634
Qy 646 ---LSEA-----THSMALTFDPVSGAFCP 666
Db 635 DQALSEALSVASQNLTGRIWGEHRPRFTHPLATOFPANAGLLNP 679

RESULT 30
Sequence 3, Application US/07935312
Patent No. 5320948

GENERAL INFORMATION:
APPLICANT: Iwami, Morita
APPLICANT: Aramori, Ichiro
APPLICANT: Fukagawa, Masao
APPLICANT: Isogai, Takao
APPLICANT: Kojo, Hitoshi
TITLE OF INVENTION: CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/935, 312
FILING DATE: 1990826
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5320946man F.
REGISTRATION NUMBER: 24, 618
REFERENCE/DOCKET NUMBER: 18-769-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 486-2347
TELEFAX: (703) 486-2347
TELELEX: 248855 OBLT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-935-312-3

Query Match 1.6%; Score 102; DB 1; Length 774;
Best Local Similarity 20.6%; Pred. No. 1.2;
Matches 145; Conservative 77; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--ACNAARBERGFSRSGQPPDGAETTGBE--ICTR---LGLEPENTILYLVTTAL 161
Db 70 LTRRKALGRAENLG--AEEAADILYLRLGNEKVERDFEALGVAKD-----M 117
Qy 162 FKEAVFMNVFLHFLYGLDLVHNGDVIRIPLPVQLMPDVNRLVPDPFNTH---R 216
Db 118 LRAVAGNAFLAGA-----PL PVEYGLGAE---PEPWEPHSLAVMR 159
Qy 217 SIGEGFVYPTPFYNTGLCHLIHDCTVAPNALVRVNTAV---ARGAHHIAFDENHEG 272
Db 160 RLG-----LLMGSUWPKLWRMLALPVUGAANALKURDYDDGRD 197
Qy 273 AV-IPPDITYTYFQSSSSCTTARGARRDNVNSTSKPPEQQGFER---RLAS---IM 322
Db 198 LLCPGGAEDRLEADLTLRPAVDALLKAMGDASDAGGGNNNWAVGRTATGRPL 257
Qy 323 AADTAHALHAVIYNTGIVYETPTDIKEWPMPFIGMEGTLPRLNALSYTARVAGVGMVFS 382
Db 258 AGDPHRVFEI---PGMYAQPHLACDRFDN-IGL---TVP-----GVGFPHFA 298
Qy 383 PNSA-----LYLTVEDSGMT-----AKDGGGPSPENRP 412
Db 299 HNGKVAYCITHAFMDIHDDLUQPAGEGTTARFGNDFFBPAVNSRDRTAVGGAADREDDIV 358
Qy 413 YQFASPHLAAANPOTRDGEVFLSSGTSGSTSNTFEDVYLALLCGFAPLALARFLYLERCD 472
Db 359 ETRHGPVIAGDP--RDGAALTLSRVQFETLSDFDCLTRMP--GASTVAGLY----D 407
Qy 473 AGAFTG--GH---GDAKXCVTGTFDSELPCLSCLEKHTRPAVCAHTTVHLR----ORMP 521
Db 508 ATRGGLIDNLVADEVASSIGHLYRARVSRSRPRENGWAVPWCNSGEHWGWHIPAMP 467
Qy 522 RFQGATROPIGVFTMNQY-----SDCDPLGNYAH-----LILRKPGDQTE 564
Db 550 DAAAATHADLSP----HYGLLRRRLREALGARDSSAEEGRMLVANDGRMDAASEVASA 574
Qy 609 HPTPRILDT---RARIBETTTQ-----FMKVVLVETDVKIREG---645
Db 635 YNAPRPAALTIVTPSGLIEAISHPPAAYARGVSPQGQWWAVPTLRLDDAGMLKGNSW 634
Qy 646 ---LSEA-----THSMALTFDPVSGAFCP 666
Db 679 DQALSEALSVASQNLTGRIWGEHRPRFTHPLATOFPANAGLLNP 679
Qy 713 YQFAGPHLAAQPHLACDRFDN-IGL---TVP-----GVGFPHFA 298
Db 758 AGDPHRVFEI---PGMYAQPHLACDRFDN-TGL---TVP-----GVGFPHFA 298
Qy 793 PNSA-----LYLTVEDSGMT-----AKDGGGPSPENRP 412
Db 800 HNGKVAYCITHAFMDIHDDLUQPAGEGTTARFGNDFFBPAVNSRDRTAVGGAADREDDIV 358
Qy 823 AADTAHALHAVIYNTGIVYETPTDIKEWPMPFIGMEGTLPRLNALSYTARVAGVGMVFS 382
Db 859 ETRHGPVIAGDP--RDGAALTLSRVQFETLSDFDCLTRMP--GASTVAGLY----D 407
Qy 893 PNSA-----LYLTVEDSGMT-----AKDGGGPSPENRP 412
Db 900 HNGKVAYCITHAFMDIHDDLUQPAGEGTTARFGNDFFBPAVNSRDRTAVGGAADREDDIV 358
Qy 939 ETTRHGPVIAGDP--RDGAALTLSRVQFETLSDFDCLTRMP--GASTVAGLY----D 407
Db 973 AGAFTG--GH---GDAKXCVTGTFDSELPCLSCLEKHTRPAVCAHTTVHLR----ORMP 521

408 ATRGQLLIDNLVAGDVASSIGHLYRARVSRRPENGWILVPGMSGEHEWRGNTIPHEAMP 467
 522 RFGQATRQPQIGVFETMNSQY-----SDCDPLGNTAYP-----LILRKPGDQTE 564
 468 R---VIDPREGIYTANNVVADDHPDYLCTDCEB----PYRAERIMRLVANPAFAWD 519
 565 AAKATMDQTYRATLERLFDLEQERLLDGA- POSSEELSSIV-----D 608
 520 DAAAIIHADTLSP----HYGLLERRLEALGARDSSAEGLRQMLVANDGRMDAASEVASA 574
 609 HPTPERILDPL--RARIBETTQ-----FMKVLTVERTDYKIREG-- 645
 575 YNAFRAALTRLVDTDRSGLGAISSHFFAAVAPGVSPQQYWWAVPTLRLDDAGMLKGNSW 634
 646 ---LSEA-----THSMALTFDPYSGAFCP 666
 635 DQAUSEALSVASQNLTGRISSMGEEHRPRFTPLAQFPANAGLLNP 679
 652 RESULT 31
 US 08-633-760-50
 Sequence 50, Application US/08633760
 Patent No. 5804429
 GENERAL INFORMATION:
 APPLICANT: NIWA, MINEO
 APPLICANT: SAITO, YOSHIMASA
 APPLICANT: FUJIMURA, TAKAO
 APPLICANT: ISHII, YOSHINORI
 APPLICANT: NOGUCHI, YUJI
 TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
 ADDRESSER: P. C.
 STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/633,760
 FILING DATE: 01-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 18-929-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEX: 248955 OPAT UR
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 774 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 Query Match 1 6%; Score 102; DB 1; Length 774;
 Best Local Similarity 21.2%; Pred. No. 1.2; Mismatches 73; Indels 238; Gaps 38;
 Matches 149; Conservative 73; Mismatches 243; Indels 238; Gaps 38;
 109 LTR - ACNAAERERGFSRCQCQPPVDAVETGAE - ICTR -- LGLEPENTILYVVTAL 161
 70 LTRRKALGRAEWLG---AFAAEADLVLRRIGMERYCRDFEALGVEAHD-----M 117

Qy 162 FKKEAVFMVNVLHYGLDVKVHTNGDVTRIPPFOLMPDVNRLLVPDFNTNH----R 216
 Db 118 LRAYVGNAFLASGA-----PL-PVEYLGAE - -PEWEWPWHISAVMR 159
 Qy 217 SIGEGFVYPTPFNTGLCHLIDHCYIAPM - -AVALYRVENNTAVARGAAHLAEDENHEGAV 274
 Db 160 RLGD-----LLLGSVWFKLWRALALPV----VGAANALKRYDDGGRDL 199
 Qy 275 -LPDDITYFQSSSGITTAGRNRNDUNSTS KPSPGGFER -----RLAS - -IMA 324
 Db 200 CIPPGAEADRLEAIDLTRPAVDALKAMGGDASDAAGGGSNNWAVAPERTATGRPILAG 259
 Qy 325 DTALHAEVIFNTGYYEETPTDIKEWPMF GMEGTIL PRUNALGTSYTAvgVIGANVFSNP 384
 Db 260 DPHRYVEI --PGYAAQHLLACDRFDN - IGL - TVP-----GVPGPPHFAIN 300
 Qy 385 SA-----LYLTVEEDSGMTB-----AKDGGPGPSFNRFYQ 414
 Db 301 GKVAYCVTHAFMDTHDLYEQFACEGRTAFGNDPEPVAWSRDIATVGRGADREDIVET 360
 Qy 415 FAGPHLAANPQTDRDGHVLSQSSTGSSNTESFYDYLALICGFGRPLLARLFLYLERCDAG 474
 Db 361 RHGPVIAGPB--RDGAALTLSRVOFAETDLSFCLTTRMP--GASTVQAQLY----DAT 409
 Qy 475 AFTG - GH ---GDALKVYTGTPOSEIPSCLSERHTRP CAHTVHLR-----QRMPPF 523
 Db 410 RGWGLIDHNLVAGDVAGSIGHLYVARVSRPRENGWLVPGWSGEHENRGWIHEAMP - 468
 Qy 524 GOA-TRPQIGVFGTMNSQY-----SDCDPLGNYAP-----LILRKPGDQTEAA 566
 Db 469 --VDPDGGIITVANRNVADDHDYLCTDCHP----PYRABIMKLVLYNPAFVDA 521
 Qy 567 KATNQDTYBTLERLFDLEQERLLDGA - -PCSSSEGLOSSIV-----DHP 610
 Db 522 AATHADTLSP----HVGLLRLREALGARDSSAEGLQMLVADGRMDAASEVASA 576
 Qy 611 TFRRLDLT -- RARIEQTTO-----FMKVLTVERTDYKIREG---- 645
 Db 577 AFRALDTLVTDRGQEAQISHPPFAAVAPGVSPQGVNWAVPTLRLDDAGMLKCSWSDQ 636
 Qy 646 -LSEA-----THSMALTFDPYSGAFCP 666
 Db 637 ALSELSVASONLTORSMGEERPRFTPLAQTPAWAGLNP 679
 RESULT 32
 US-08-011-870-1
 ; Sequence 1, Application US/08019870
 ; Patent No. 5326613
 ; GENERAL INFORMATION:
 ; APPLICANT: NIWA, MINEO
 ; APPLICANT: YOSHIMASA, SAITO
 ; APPLICANT: SASAKI, HITOSHI
 ; APPLICANT: ISHII, YOSHINORI
 ; TIME OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
 ; ADDRESSER: P. C.
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0., Version #1.25
 ; APPLICATION NUMBER: US/08/019,870
 ; FILING DATE: 1983-01-19
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 18-929-0 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 413-3000
 ; TELEX: 248955 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 774 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; Query Match 1 6%; Score 102; DB 1; Length 774;
 ; Best Local Similarity 21.2%; Pred. No. 1.2; Mismatches 73; Indels 238; Gaps 38;
 ; Matches 149; Conservative 73; Mismatches 243; Indels 238; Gaps 38;
 ; 109 LTR - ACNAAERERGFSRCQCQPPVDAVETGAE - ICTR -- LGLEPENTILYVVTAL 161
 ; 70 LTRRKALGRAEWLG---AFAAEADLVLRRIGMERYCRDFEALGVEAHD-----M 117

ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5336613man F.
 REFERENCE/DOCKET NUMBER: 24-618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 248855 OPAT UR
 SEQUENCE CHARACTERISTICS:
 LENGTH: 773 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-019-870-1

Query Match 1.6%; Score 101.5; DB 1; Length 773;
 Best Local Similarity 21.9%; Pred. No. 1.4; Gaps 19;
 Matches 91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;

US-08-019-870-6

Query Match 1.6%; Score 101.5; DB 1; Length 773;
 Best Local Similarity 21.9%; Pred. No. 1.4; Gaps 19;
 Matches 91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;

Query Match 1.6%; Score 101.5; DB 1; Length 773;
 Best Local Similarity 21.9%; Pred. No. 1.4; Gaps 19;
 Matches 91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;

Query 372 VAGVIGAMWFSNSA-----LYLTTEVEDSGMT-----AK 401
 Db 287 VEGVGPFPFAIRGKVAXVTHAFMDIHDLYLEQFAGERGTRAFGNDFEPVAWSRDRIAV 346

Qy 402 DGGGPSFRFRYQFAGPHIAYAPOTDGGHVLSSQSITGSNTSEESDYALICGFAPLI 461
 Db 347 RGGADREFDIVETRHGPVIAQDP--RDGAALTLSRSQFAETDLSFCLTMP--GASTV 401

Qy 462 ARLLFYLERCDAGFTG--GH---GDAKYTTGTGFDSEIPCSLCEKHTPVAHTTVHR 515
 Db 402 AQLY----DATRGWGLIDHNLVAGDVASIGHLYARVSPRENGWLPVGWSGEHE 455

Qy 516 LR----QRMPIRGQATQPIGYFGTMNSQY-----SDCDPLGNAYF-----553
 Db 456 WRGMIPHEAMPR--VIDEPPGIVTVANVVADDHPDYLCTDCHP----PYRAERIMK 507

Qy 554 LILRKPGDQTEAAKATMOTDYLRTALERLFLDEQERULDRGA--PCSEGGLSSVIV----553
 Db 508 RLVANPAFAVDDAAAHADTLSP----RVGLLRRLEAIGRDSSAEGLRQLVAWDG 562

Qy 608 -----DHPTRRLLDTL--RARIEQTTQ-----FMKVLTET 637
 Db 563 RMDAASEVASYNAFRALLTRLDRSIEQAISSHPPFAAVAPVSQSQWWAVPTLIRD 622

Qy 638 RDYKREG----LSEA-----THSMALTFDPYSGAFCP 666
 Db 623 DDAGMLKGWSWDQALSEALSVASQNLTRGSWGBEHRPFTHPLATQPAWAGLNP 678

RESULT 33
 US-08-019-870-6
 Sequence 6, Application US/08019870

GENERAL INFORMATION:
 APPLICANT: NIWA, MINEO
 APPLICANT: YOSHIMASA, SAITO
 APPLICANT: SASAKI, HITOSHI
 APPLICANT: ISHII, YOSHINORI
 TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESSSEE: P.C.
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

RESULT 34
 US-08-019-870-9
 Sequence 8, Application US/08019870
 Patent No. 5336613
 GENERAL INFORMATION:
 APPLICANT: NIWA, MINEO
 APPLICANT: YOSHIMASA, SAITO
 APPLICANT: SASAKI, HITOSHI
 APPLICANT: ISHII, YOSHINORI
 TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESSSEE: P.C.
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/019,870
 FILING DATE: 19930219
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5336613man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 18-791-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 774 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-08-019-870-8

Query Match 1.6%; Score 101.5; DB 1; Length 774;
 Best Local Similarity 21.9%; Pred. No. 1.4; Mismatches 41; Indels 145; Gaps 19;
 Matches 91; Conservative 41; US-08-019-870-11

Qy 372 VAGTIGAMYFSPNSA-----LYLTIVEDSGMTB-----AK 401
 Db 288 VPGPGPFPAHNGKAVSUTHMDIHDLYQFAGSRTARFGNDPEPWAWSRDIAY 347
 Qy 402 DGGGPSFNRFYQAGPHLAANPOTDRDGHVLSQSSTGSSNTFSDYVLA 461
 Db 348 RGGADREFDVETHGPVIAGD----RDAALTLRSVQFAETLSDFLTRMP-GASTV 402
 Qy 462 ARLLFYLERDAGATG-GH---GDAIKYVGTGTFSEIPCSLCEKHTRYCAHTTYVR 515
 Db 403 AQLY----DATRGWGLIDHNLYAGDVAGSIGHLVRARPSSPRENGWLPYEGWSGEHE 456
 Qy 516 LR---QRMPRFQATOQTFQIGVGTGMNSQY-----SDCDPLQNYAPY-----
 Db 457 WRGNTPHEAMPF---VIDPGGIVLVTANNRYYVADDHPDYCTCUP----PRAERIMK 508
 Qy 554 LILRKPGDQTEAKATMDDQYRATERLRLTDLEBDRDGA-PCSSBGLSSVIV---- 607
 Db 509 RLVANPAFAVDAAARIADYLSP----HVGLLRRRLBAAGDDSAEGLRQMLVAWDG 563
 Qy 608 -----DHPTFRRLDTL--RARIEOTTQ----FMKVILVET 637
 Db 564 RMDAASEVASYNAFRAALTRLTDISGLEQAIISHPFAAVAPGVSPQGOVWWAVPTLIRD 623
 Qy 638 RDYKREG----LSEA-----THSMWALTFDPYSGAFCP 666
 Db 624 DDAGMLKGNSWDQASLEAVASQNLTRGAWGEBEHRPRTHPLATQFPAWAGLNP 679

RESULT 35
 US-08-019-870-11
 Sequence 11, Application US/08019870
 Patent No. 5336613
 GENERAL INFORMATION:
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 APPLICANT: NIWA, MINEO
 APPLICANT: YOSHIMASA, SAITO
 APPLICANT: SASAKI, HITOSHI
 APPLICANT: ISHII, YOSHINORI
 TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE

STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOCS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/019,870
 FILING DATE: 19930219
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5336613man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 18-791-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 774 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-08-019-870-11

Query Match 1.6%; Score 101.5; DB 1; Length 774;
 Best Local Similarity 21.9%; Pred. No. 1.4; Mismatches 41; Indels 145; Gaps 19;
 Matches 91; Conservative 41; US-08-019-870-11

Qy 372 VAGTIGAMYFSPNSA-----LYLTIVEDSGMTB-----AK 401
 Db 288 VPGPGPFPAHNGKAVSUTHMDIHDLYQFAGSRTARFGNDPEPWAWSRDIAY 347
 Qy 402 DGGGPSFNRFYQAGPHLAANPOTDRDGHVLSQSSTGSSNTFSDYVLA 461
 Db 288 VPGPGPFPAHNGKAVSUTHMDIHDLYQFAGSRTARFGNDPEPWAWSRDIAY 347
 Qy 402 DGGGPSFNRFYQAGPHLAANPOTDRDGHVLSQSSTGSSNTFSDYVLA 461
 Db 348 RGGADEFDIVTRGPVIAGD----RDGAALTLRSVQFAETLSDFLTRMP-GASTV 402
 Qy 462 ARLLFYLERDAGATG-GH---GDAIKYVGTGTFSEIPCSLCEKHTRYCAHTTYVR 515
 Db 403 AQLY----DATRGWGLIDHNLYAGDVAGSIGHLVRARPSSPRENGWLPYEGWSGEHE 456
 Qy 516 LR---QRMPRFQATOQTFQIGVGTGMNSQY-----SDCDPLQNYAPY-----
 Db 457 WRGNTPHEAMPF---VIDPGGIVLVTANNRYYVADDHPDYCTCUP----PRAERIMK 508
 Qy 554 LILRKPGDQTEAKATMDDQYRATERLRLTDLEBDRDGA-PCSSBGLSSVIV---- 607
 Db 509 RLVANPAFAVDAAARIADYLSP----HVGLLRRRLBAAGDDSAEGLRQMLVAWDG 563
 Qy 554 LILRKPGDQTEAKATMDDQYRATERLRLTDLEBDRDGA-PCSSBGLSSVIV---- 607
 Db 509 RLVANPAFAVDAAARIADYLSP----HVGLLRRRLBAAGDDSAEGLRQMLVAWDG 563
 Qy 608 -----DHPTFRRLDTL--RARIEOTTQ----FMKVILVET 637
 Db 564 RMDAASEVASYNAFRAALTRLTDISGLEQAIISHPFAAVAPGVSPQGOVWWAVPTLIRD 623
 Qy 638 RDYKREG----LSEA-----THSMWALTFDPYSGAFCP 666
 Db 624 DDAGMLKGNSWDQASLEAVASQNLTRGAWGEBEHRPRTHPLATQFPAWAGLNP 679

Search completed: June 3, 2004, 07:15:17
 Job time : 34 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM Protein - protein search, using SW model

Run on: June 3, 2004, 07:04:28 ; Search time 553 Seconds
 (without alignments)
 612,026 Million cell updates/sec

Title: US-09-769-699-2

Perfect score: 6294
 Sequence: 1 MENTQKTVTPGPIGVTA,.....DELPDLGIPKHNIGNITEM 1203

Scoring table: BLOSUM62
 Gapext 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters:
 Minimum Match 0%
 Maximum Match 100%

Listing first 100 summaries
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Database : Published Applications AA:*

1: /cgns2_6_ptodata/1/pubpaa/us00_pubcomb.pep:*

2: /cgns2_6_ptodata/1/pubpaa/us00_pubcomb.pep:*

3: /cgns2_6_ptodata/1/pubpaa/us06_pubcomb.pep:*

4: /cgns2_6_ptodata/1/pubpaa/us06_pubcomb.pep:*

5: /cgns2_6_ptodata/1/pubpaa/us07_pubcomb.pep:*

6: /cgns2_6_ptodata/1/pubpaa/pctms_pubcomb.pep:*

7: /cgns2_6_ptodata/1/pubpaa/us08_pubcomb.pep:*

8: /cgns2_6_ptodata/1/pubpaa/us08_pubcomb.pep:*

9: /cgns2_6_ptodata/1/pubpaa/us09_pubcomb.pep:*

10: /cn2_6_ptodata/1/pubpaa/us09_pubcomb.pep:*

11: /cn2_6_ptodata/1/pubpaa/us09_pubcomb.pep:*

12: /cn2_6_ptodata/1/pubpaa/us09_new_pub.pep:*

13: /cgns2_6_ptodata/1/pubpaa/us10_pubcomb.pep:*

14: /cn2_6_ptodata/1/pubpaa/us10_pubcomb.pep:*

15: /cn2_6_ptodata/1/pubpaa/us10c_pubcomb.pep:*

16: /cgns2_6_ptodata/1/pubpaa/us10_new_pub.pep:*

17: /cn2_6_ptodata/1/pubpaa/us10_new_pub.pep:*

18: /cgns2_6_ptodata/1/pubpaa/us60_pubcomb.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6294	100.0	1203	12	US-09-769-699-2
2	3054	48.5	1452	13	US-10-050-673-2
3	3015.5	47.9	1196	14	US-10-237-551-000
4	3015.5	47.9	1196	14	US-10-237-551-000
5	3015.5	47.9	1196	14	US-10-237-551-000
6	789	12.5	274	14	US-10-237-551-331
7	736	11.7	248	14	US-10-237-551-330
8	123.5	2.0	850	14	US-10-156-761-9121
9	123.5	2.0	2597	12	US-10-154-351-34
10	123	2.0	1074	12	US-10-206-576-358
11	123	2.0	1074	12	US-10-206-576-394
12	121	1.9	2358	12	US-10-282-122A-45763
13	120.5	1.9	2597	9	US-09-905-129-2
14	120.5	1.9	2597	9	US-09-905-129-10
15	120.5	1.9	2597	9	US-09-905-129-13

Result No.	Score	Query Match	Length	DB ID	Description
1	6294	100.0	1203	12	US-09-769-699-2
2	3054	48.5	1452	13	US-10-050-673-2
3	3015.5	47.9	1196	14	US-10-237-551-000
4	3015.5	47.9	1196	14	US-10-237-551-000
5	3015.5	47.9	1196	14	US-10-237-551-000
6	789	12.5	274	14	US-10-237-551-331
7	736	11.7	248	14	US-10-237-551-330
8	123.5	2.0	850	14	US-10-156-761-9121
9	123.5	2.0	2597	12	US-10-154-351-34
10	123	2.0	1074	12	US-10-206-576-358
11	123	2.0	1074	12	US-10-206-576-394
12	121	1.9	2358	12	US-10-282-122A-45763
13	120.5	1.9	2597	9	US-09-905-129-2
14	120.5	1.9	2597	9	US-09-905-129-10
15	120.5	1.9	2597	9	US-09-905-129-13

16	120.5	1.9	2597	9	US-09-991-630-2
17	120.5	1.9	2597	9	US-09-991-630-13
18	120.5	1.9	2597	12	US-10-454-351-2
19	120.5	1.9	2597	12	US-10-454-351-10
20	120.5	1.9	2597	12	US-10-454-351-13
21	120.5	1.9	2597	12	US-10-454-351-13
22	120.5	1.9	2597	12	US-09-729-485A-2
23	120.5	1.9	2597	12	US-09-729-485A-10
24	120.5	1.9	2597	12	US-09-729-485A-13
25	120.5	1.9	2597	12	US-09-802-318-2
26	120.5	1.9	2597	12	US-09-802-318-10
27	120.5	1.9	2597	12	US-09-902-318-13
28	120	1.9	5245	14	US-10-329-079-11
29	118	1.9	452	12	US-10-425-114-71520
30	118	1.9	19608	15	US-10-094-846A-8
31	114.5	1.8	1479	12	US-10-231-156A-325
32	114.5	1.8	1496	12	US-10-211-462-87
33	114.5	1.8	1496	14	US-10-021-660-125
34	114.5	1.8	1496	14	US-10-331-496A-28
35	114.5	1.8	1498	12	US-10-276-74-397
36	114.5	1.8	1498	12	US-10-243-552-899
37	113.5	1.8	1477	14	US-10-274-583-20
38	113	1.8	1682	12	US-10-282-122A-64702
39	113	1.8	1787	12	US-10-180-62625
40	113	1.8	2505	12	US-10-205-331-20
41	112	1.8	943	12	US-10-282-122A-68197
42	112	1.8	3868	16	US-10-461-194-103
43	112	1.8	6620	16	US-10-080-334-950
44	112	1.8	3069	14	US-10-408-765A-291
45	111.5	1.8	4317	12	US-10-282-122A-67862
46	111	1.8	5215	9	US-09-861-219-2
47	111	1.8	5215	9	US-09-86-846-2
48	111	1.8	5215	10	US-09-988-384B-2
49	111	1.8	5215	10	US-09-836-821-7742
50	111	1.8	5215	14	US-10-271-889-45
51	10.5	1.7	3069	12	US-09-172-363-246
52	110	1.7	771	16	US-10-389-166-934
53	110	1.7	784	12	US-10-282-122A-68623
54	110	1.7	7039	13	US-10-382-122A-77942
55	109.5	1.7	2630	13	US-10-077-130-2
56	109.5	1.7	7968	13	US-10-177-130-5
57	109	1.7	3069	12	US-10-267-50-372
58	108	1.7	386	12	US-10-424-519-20597
59	108	1.7	499	14	US-10-369-193-10577
60	108	1.7	8026	14	US-10-132-134-12
61	107.5	1.7	905	14	US-10-160-174-677-8
62	107	1.7	1279	12	US-10-332-288-6
63	107	1.7	3298	15	US-10-120-301-511
64	106.5	1.7	1299	14	US-10-156-761-12449
65	106.5	1.7	2448	12	US-10-210-172-48
66	106.5	1.7	3298	12	US-10-132-172-50
67	106.5	1.7	3298	14	US-10-160-175-16
68	106.5	1.7	3298	14	US-10-174-677-8
69	106.5	1.7	3298	15	US-10-120-301-511
70	105.5	1.7	707	14	US-10-156-761-997-9
71	105.5	1.7	1052	16	US-10-389-566-608
72	105.5	1.7	1563	15	US-10-334-143-34
73	105.5	1.7	1967	14	US-10-219-834-85
74	104.5	1.7	635	16	US-10-951-847-55
75	104.5	1.7	1471	8	US-08-811-519A-1
76	104.5	1.7	1967	14	US-10-340-154-8
77	104.5	1.7	3530	12	US-10-396-115-1101
78	104.5	1.7	6304	14	US-10-147-0-16-16
79	104.5	1.7	3192	14	US-10-332-134-10
80	104.5	1.7	495	12	US-10-325-114-65528
81	104	1.7	83	12	US-10-382-122A-5721
82	103.5	1.6	103.5	12	US-10-043-555-920
83	103.5	1.6	1750	12	US-10-043-555-920
84	103.5	1.6	1050	12	US-10-082-122A-7119
85	103	1.6	3472	13	US-10-034-623-4
86	103	1.6	3472	13	US-10-027-801-4
87	103	1.6	3472	14	US-10-027-801-4
88	103	1.6	3472	14	US-10-027-801-4

RESULT 1
 US 09-769-699-2
 ; Sequence 2, Application US/09769699
 ; Publication No. US20010039051A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Silverstein, Saul J.
 ; APPLICANT: Lungu, Octavian
 ; APPLICANT: Gershon, Anne A.
 ; ATTORNEY: Annunziato, Paula W
 ; FILE REFERENCE: 0575/6115-A
 ; CURRENT APPLICATION NUMBER: US/09-769,699
 ; CURRENT FILING DATE: 2002-04-22
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO: 2
 ; LENGTH: 1203
 ; TYPE: PRT
 ; ORGANISM: Varicella zoster
 ; US-09-769-699-2.

Query Match Score 6294; DB 12; Length 1203;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MENTOKTVYPTGPIGYYYACRVDLDEIISFLAARSTDSDLPLMRNITVEKFTS	60
Db	1	MENTOKTVYPTGPIGYYYACRVDLDEIISFLAARSTDSDLPLMRNITVEKFTS	60
Qy	61	SLAVYSGARTTGLAGATIKLKLTTSHFYPVYFHGGKHLPSAAPNLTRACNAARER	120
Db	61	SLAVYSGARTTGLAGATIKLKLTTSHFYPVYFHGGKHLPSAAPNLTRACNAARER	120
Qy	121	GFSRCGPPYDGAETTGABICPGLIGBENTILLYVTALEKCAEVNCFVHYGGID	180
Db	121	GFSRCGPPYDGAETTGABICPGLIGBENTILLYVTALEKCAEVNCFVHYGGID	180
Qy	181	VHNGDVTIRIPLFPVQLNPMDPNRLVPDPFNTHRSIGEGFYTPPTNTGLCHLHD	240
Db	181	VHNGDVTIRIPLFPVQLNPMDPNRLVPDPFNTHRSIGEGFYTPPTNTGLCHLHD	240
Qy	241	VIAPMAVALVRNVTAVARGAAHLAFDENHEGAVLPPDTIYTTFQSSSGTTARGARN	300
Db	241	VIAPMAVALVRNVTAVARGAAHLAFDENHEGAVLPPDTIYTTFQSSSGTTARGARN	300

RESULT 2
 US-10-050-673-2
 ; Sequence 2, Application US/10050673
 ; Publication No. US200201033A1
 ; GENERAL INFORMATION:
 ; APPLICANT: David M. Knipe
 ; APPLICANT: Travis J. Taylor
 ; APPLICANT: Elizabeth McNamee
 ; TITLE OF INVENTION: Replication-Competent Virus Expressing A
 ; TITLE OF INVENTION: Fusion Protein
 ; FILE REFERENCE: HU98-05
 ; CURRENT APPLICATION NUMBER: US/10/050,673
 ; CURRENT FILING DATE: 2002-01-16
 ; PRIOR APPLICATION NUMBER: US/09/127,227
 ; PRIOR FILING DATE: 1998-07-31
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 1452

ALIGNMENTS

Qy	481	GDALKYVGTGTFDSIPCSICEKTRPCAAHTVHRIFORMPFFGOAQRQPIGEFGTNNSQ	540
Db	481	GDALKYVGTGTFDSIPCSICEKTRPCAAHTVHRIFORMPFFGOAQRQPIGEFGTNNSQ	540
Qy	541	YSDCDPLGNAYAPYLILRKPGDQTEAAKATMDTYRATERLFLDEQRLDORGAPCSSE	600
Db	541	YSDCDPLGNAYAPYLILRKPGDQTEAAKATMDTYRATERLFLDEQRLDORGAPCSSE	600
Qy	541	YSDCDPLGNAYAPYLILRKPGDQTEAAKATMDTYRATERLFLDEQRLDORGAPCSSE	600
Db	541	YSDCDPLGNAYAPYLILRKPGDQTEAAKATMDTYRATERLFLDEQRLDORGAPCSSE	600
Qy	601	GLOSSVIVDHTPFRILDCLRARLEOTTOQMVKLVETDVKIREGLSEATHSMALTFDPY	660
Db	601	GLOSSVIVDHTPFRILDCLRARLEOTTOQMVKLVETDVKIREGLSEATHSMALTFDPY	660
Qy	661	SGAFCPTINFLVRKTHLAVQDIALSQCCHCVFVQQVGRNFQPVLRREFDLNG	720
Db	661	SGAFCPTINFLVRKTHLAVQDIALSQCCHCVFVQQVGRNFQPVLRREFDLNG	720
Qy	721	GFISTRITVTLSEGPPVSAAPNPTLQDAPAGRIFDDGLARYSVETVIRKVRVFSGN	780
Db	721	GFISTRITVTLSEGPPVSAAPNPTLQDAPAGRIFDDGLARYSVETVIRKVRVFSGN	780
Qy	781	CTNLSBEAARLVLGASATOQERGVDMHAGLFLKFQFHGLLPRGMPPNSKSPNPOW	840
Db	781	CTNLSBEAARLVLGASATOQERGVDMHAGLFLKFQFHGLLPRGMPPNSKSPNPOW	840
Qy	841	FMTLQLQNMQPADLTHEETTIAAVKRTEEYAAINFNLPPTCIGELAQFTYMANLIK	900
Db	841	FMTLQLQNMQPADLTHEETTIAAVKRTEEYAAINFNLPPTCIGELAQFTYMANLIK	900
Qy	901	YCDHSQLINTLTSITGARRPROPSVLUWIRDKDTSADIEQAKALLEKTNLPELW	960
Db	901	YCDHSQLINTLTSITGARRPROPSVLUWIRDKDTSADIEQAKALLEKTNLPELW	960
Qy	961	TIAFSTHLYRAAMNQRPMVYLGISISKHGAAGNRVRQAGNWSGLANGKRNVCPLFTFD	1020
Db	961	TIAFSTHLYRAAMNQRPMVYLGISISKHGAAGNRVRQAGNWSGLANGKRNVCPLFTFD	1020
Qy	1021	RTRRFIIACPRGGFICPTOPSGNRETLSDQVGIJIVSGGANYQLAJATVYRAVGAR	1080
Db	1021	RTRRFIIACPRGGFICPTOPSGNRETLSDQVGIJIVSGGANYQLAJATVYRAVGAR	1080
Qy	1081	AQHMADFDSLTDDEFLARLDEELHDQIQTLETPTWTEGALEAKVILDEKTAGDET	1140
Db	1081	AQHMADFDSLTDDEFLARLDEELHDQIQTLETPTWTEGALEAKVILDEKTAGDET	1140
Qy	1141	PTNLAFNFDSCBPHDTSNYLNNSGSNTSGSNTVPGLSIPKIGHGNIT	1200
Db	1141	PTNLAFNFDSCBPHDTSNYLNNSGSNTSGSNTVPGLSIPKIGHGNIT	1200
Qy	1201	MEM 1203	
Db	1201	MEM 1203	

; TYPE: PRT
; ORGANISM: herpesvirus
; US-10-050-673-2

Query Match 48.5%; Score 3054; DB 13; Length 1452;
Best Local Similarity 49.8%; Pred. No. 5e-294;
Matches 609; Conservative 200; Mismatches 366; Indels 48; Gaps 17;

Qy 1 MENTOKTVT---VPRPIGLVY--ACRVEDLDLIESFLAARSDSDLALPLMRNLTVE 55
Db 1 METKSKTATTIKVPPCPGLVYARACPSGIEL--LAISLARSQDADAVAPLVVGTV 58

Qy 56 KTFITSLAVSVSAGARTTGLAGAGITRKLTTTHFYPBFVFGREVLPSAAAPNTTATNA 115
Db 59 SGFEANAVVYUGSRTGTLGGTAVSULKUTPHEYSSVVFPHGRHLDPSTQAPNTRCLER 118

Qy 116 ARERFGFSRCQCGPPVGDGAVETTGAACTRLGLEPENTILYLVTAFLKEAVFMCNVFLHY 175
Db 119 ARRHFQFSDFDTPRGILKHETGEALCERGLDPRALLLVLVTEBFRKAVCINNTFLH 178

Qy 176 GGDLIWHINGDVIRPLEFVQLQFLPDVNELVPDPDNTHRSIGEGFYPTPFYNTGLCH 235
Db 179 GGSDKTYTIGAEVHRIPVPIVQFLNMDPSVIAIBFNRSIGENFTPLPFPNRPINR 238

Qy 236 LIHDCVTAPEAHVLYRNTAVARGAHLLDENHEGAIVPFDITYTQSSESSGTTAR 295
Db 239 LLFEATVGPAAVLCRNVDAVARAAAHAFDENHEGAALPADETTFAEASQG--KTPR 296

Qy 296 GARNDVNSTSKPSPGGFERLASIMAIDLHALDEVINTGIVEETPDTIKEWPMFMGM 355
Db 297 GCR----DGSGKGPRGGFERPLASMAGAAALESTISMAVEPEPPDISAPLCEQ 351

Qy 356 EGTLPLRNALGSYTARVAGTIGAMYFSPNALSALYTEDVSDGMTEAKDGGPGPSNRFYOF 415
Db 352 DTAARANAVGAYLARAAGLGAMVFSNSALHLTEVDGGPDKDHSK-PSTYRFFLY 410

Qy 416 AGPHLAAANPQCDRDGHVU-----SSQSTGSNTTEFSVSYDYLALICGFGBPLIARLLFY 468
Db 411 PGTHVAANPQVDREGHVUPGFEGRPPAPLNGTQ-BFAGHLMICGFSALLAKMLPFL 469

Qy 469 ERCDAGAFTGGHG-DALKYVGTGTDSEBIPSCLCEKTRPVCAHTVHLRORMPRFGQT 527
Db 470 ERCDGGTVGRQEMDYVADSNCQDVPCNLCTPTRACVHTLMLRARHFKPASA 529

Qy 528 RQPIGVGTMSQYSDDPLQNYAPYLILRKPGDQEAAKATMDQTYTRILERFIDEQ 587
Db 530 RGAIGVGTMSYMSDCDVLYNYAASALKR-ADGSETARTIMQTYTRATERWMALET 589

Qy 588 ERLDRQAPCSSEGGLSSVIVDHPTRRILDTLRARLEOTTIQFMKVLTREDYKIREGUS 647
Db 589 LQYDQAVPANTGRLETITTRREALHTVVNNRQDVREQLRNLYVECRNFKERDGLG 648

Qy 648 BATHSMALTEDPYSGACFCPTINFLVERTHLAVYDQLASOCHCFYGOQVEGRNFRNQFO 707
Db 649 EAHNHAMSLDLYDAGCPCPQLLGRGRSNALVYDIALSQCQGVFAGSYVEGRNFRNQFO 708

Qy 708 PYLRRREVLDENGFFISTRSTTIVLSEG-PYSAAPNPTLGGDAPASRTFEDDLARYSVEV 766
Db 709 PYLRRRYDMFNGELSAKLTVALSEGAICAPSLTAGQTAAPASSFEDDVARLTGFP 768

Qy 767 RJLRVQRVVFENGCTNLSEAPARLYGLAAAYQREBKRTDMHLGALGPFLKOFHGLFP 826
Db 769 KEIRVKSRVLFAGSANASEAKARYASLQSAVOKDVKDILGPFLKOFHAAIFP 828

Qy 827 RGMPPNSKSPPNQFWTLLORNQMPAKLTHEITIIAVERFTERYAANFINLPPTCI 886
Db 829 NGKPPGSGNQNPFWTLLORNQMPAKLQPARLSREDIETIAFKKPSLDYGAINFNLAPNN 888

Qy 887 GELAQFTMANLILKYCDHSQYINTLTSITGARRPRDPSVLYHTRKDVSAAJETQA 946
Db 889 SELAMYNNQQLRYCDHSITFINTLTAIINGSRRPPSVQAAAAM--SAQGGAGLEAGA 945

Qy 947 KALLEKTENLPELWNTAFTSTHLVRAMAQNQRMVYVGLISTSKYHAGANNTRVOAGNWSG 1006

Db 946 BALMDATAHPGAWNTMSMASCNLRLRVAARPMVYVGLISTSKYHAGANNTRVOAGNWWS 1005
Qy 1007 LNGGNKNCPPLPFDTRFLIACTPREGGFCIPVTPGSSGNRETTLSQVRGIVTSGGAMVQ 1066
Db 1006 LNGGNKNCPPLPFDTRFLIACTPREGFVCAASNLUGGAHESSLCQLRGITSEGAAVA 1065

Qy 1067 LATYATVTRAVGARAOMAIDFDWLSTIDDEFLARDLSEBLHQIQTQLETPMVEGL-- 1123
Db 1066 SSYFVATVKSLOPRTQOLQIEWLALDEVLESEMMELTARALENGENSTDALLEVA 1125

Qy 1124 -PAVKILDDEKTTAGDGETPTNLIAENFD--SCBPSHDTSNTLNISNISNTSGSTVPEGKRP 1180
Db 1126 HEABALSQLGRNAGE-----VNFRDFGCE-----DDNATPFGGDPGAPGAPAGRKRA 1173

Qy 1181 PEDDELFDLSGIPKIGNITMEM 1203
Db 1174 FHEDDPFG-EGPDDKKGDLTLDM 1195

RESULT 3
US-10-200-562-200
; Sequence 200, Application US/10200562
; General Information, ; Sequence 200, Application US/10200562
; Applicant: McCown, Patrick ; Application No. US20030165819A1
; Applicant: Hosken, Nancy A. ; Inventorship Information
; Title of Invention: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; Treatment of Herpes Simplex Virus Infection ; Title of Invention
; File Reference: 210121_538C2 ; Current Application Number: US/10/200-562
; Current Filing Date: 2002-07-19 ; SEQ ID NOS: 212
; Software: FastSEQ for Windows Version 4.0 ; SEQ ID NO: 200
; LENGTH: 1196 ; TYPE: PRTR
; ORGANISM: HSV2 ; ORGANISM: HSV2
; US-10-200-562-200

Query Match 47.9%; Score 3015.5; DB 14; Length 1196;
Best Local Similarity 49.0%; Pred. No. 2.5e-200; Matches 595; Conservatve 213; Mismatches 366; Indels 41; Gaps 16;

Qy 4 TOKTUVYPTGPLGXYV--ACRVEDDLEEEISPLAARSTDSDLALLPLMRNLTVEKTPTSS 61
Db 7 TTTCVKVFPGPMLGXYVYGRCPAGLEL--LSSLISARGSDADAVAPLVLGVLTESGBEAN 64

Qy 62 LATVSGAIRTGTLGAGITKLTSHPSVYFHGGHVLPPSSAAPLTRAQNAARRFRG 121
Db 65 VAATVGSRTGLGUGTAVSLKLMPSHYPESVYFHGGHHLAPBTQAPNTRLCCRPHFG 124

Qy 122 FSRQGQPPVDPGAVETTGAEICPRGLPEENTILYLVTAFLKEAVFCNVFLHYGGDIV 181
Db 125 FADYAPRPCDLSKHTTGDALCERLGLDPRRALYLVZTEGFREAVCISNTFLHGGDKV 184

Qy 182 HINHGDIVIRIPLFPVQLPMDVNRVLPDPFNTHRS-GE GFVYPTPYNTGLCHLIDCV 241
Db 185 TIGDAEVIRIPVPLQMMDFPVRVIAFPNCNHRSGENENYPLPFPNRPLARLIEFAV 244

Qy 242 IAPMVAFLRVNTAVARGAAHLAFDENHEGAVLPPDITYTFOQSSSGTTARGARREN 301
Db 245 VGPAAVAKARNVDAVAAAHAFDENHEGALPDTTFAEASSQ--KPORGAR-- 299

Qy 302 VNSTS SKPSGGFERRLASMIMAADTALHAEVINTGIVBETPTDIKEWPMFIGEGTLPR 361
Db 300 -DAGNKGPAGGFQRLASVMGAIALESIVSMVAEDEPPDDITWPLLEQETPAA 357

Qy 362 LNAGSYTARVAGYIGAMFSPSIALYITEVEDSGMTAEKDGGPGLPSPNRFYOFAGPHLA 421
Db 358 AGAVGAYLARAAGLVGMYFSTNSALHTEVDAAGPDKDHSK-PSYRFFLVPGTHVA 416

Qy 422 ANPQTDRDGHV-----SSQSTGSNTSFVDYLALICGFGBPLIARLLFYLERCDAG 474

RESULT 5
 US-10-237-551-232
; Sequence 232, Application US/10237551
; Publication No US20030105820A1
; GENERAL INFORMATION:
; APPLICANT: Day, Craig H.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Parsons, Joseph M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
; FILE REFERENCE: 210121.538C3
; CURRENT APPLICATION NUMBER: US/10/237,551
; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO: 232
; LENGTH: 1196
; TYPE: PRT
; ORGANISM: Herpes simplex virus

US-10-237-551-232

Query Match Score 47.9%; Score 3015.5; DB 14; Length 1196;
 Best Local Similarity 49.0%; Pred. No. 2.5e-290;
 Matches 595; Conservative 213; Mismatches 366; Indels 41; Gaps 16;

Qy 4 TOKVTVTPRGPLGVY- -ACRVEDDLDEISISSLAAARSTDSDIALLPMLRNITVEKTFPTSS 61
 Db 7 TTTVKVPPGPMGVGRACPAEGL -LSSLISARSCDADAVAPAVLIVGLTVESGPEAN 64
 Qy 62 LAVVSGARTTGLAGAGITKLTKLTSHFYPSTVPHGGKHVLPSAAPNLTRACNAARERFG 121
 Db 65 VAATVGSRATGLGTAVSLKLMPHSSVYVPHGRHLAPSTQAOPNLTRICERARPHFG 124
 Qy 122 FSRQGPPYDGAVBTGAEICPBLGLEPENTLYLYTALKEAENVONVPLHYGGSDIV 181
 Db 125 FADYAPRPCLDKHETTGDALECRIGLDLDRALLYVTEGEGFEEAVCISNTPLHLGNDKV 184
 Qy 182 HINHGDVIRPLPVQLMPDVRLVPDPFTNTHRS1CEGFPYPTPYNTGLCHLHDCV 241
 Db 185 TIGDAEVHRIPVYPLQMNPDEFRIAVPFCNHRSGENENYPLPFENRPLARLFEAV 244
 Qy 242 IAPKVALVERVNITAVARGAHLAFLDENHEAVIINTGTYEETPTDIKEWMFIGMEGTLP 361
 Db 245 VGPAAVALRARNIDAVARAHHLAFLDENHEGAALPADITTAFAEASQG- -KPQRGR-- 299
 Qy 302 VNSTSXPSPSGFERRLASIMADTAHLAEVINTGTYEETPTDIKEWMFIGMEGTLP 361
 Db 300 - -DAGNKGRGGFQRLASVMAALESIYMAVEDEPPDITWPLLEGQETPAAR 357
 Qy 362 LNAGSYTARVAGVIGAMYPSNSALYLTVEVEDSGMTEAKDGGPGPSFNRYQFAGPHLA 421
 Db 358 AGAYGAYLARAAGLVGAMYFSTNSALHTEVDAGPADPKDSHK- PSFYRFLVPGTHVA 416

RESULT 6
 US-10-237-551-231
; Sequence 231, Application US/10237551
; Publication No. US20030105820A1
; GENERAL INFORMATION:
; APPLICANT: Day, Craig H.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Parsons, Joseph M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
; FILE REFERENCE: 210121.538C3
; CURRENT APPLICATION NUMBER: US/10/237,551
; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 231

LENGTH: 274
; TYPE: PRT
; ORGANISM: Herpes simplex virus
US-10-237-551-231

Query Match 7
Best Local Similarity 12.5%; Score 788; DB 14; Length 274;
Matches 153; Conservative 41; Mismatches 75; Indels 2; Gaps 1;
Qy 28 LEETSFIAARSTSDIALLPLMRNTLVEKTTTSLAVSGARTGLAGAGITLKLTTSF 87
Db 2 LEILSLSAARSQDADVAPLTLVGLTVESGPANVAVSVRSRTGIGTAVSLKMPSHY 61
Qy 98 YPSVEVTHGCKTVLBSAAPIITBACNAAREPFGESRCQQGPPDVGAETTGAEICTRIGI 147
Db 62 SPVVVPHGRHLAPSTQAPNTRCLCRAHFRGFSDYAPRCDLKHETSDALCBRLGL 121
Qy 148 EPNTILYLVTALFKRFAVFMENPVLYHGDLIVHNKGVDVRIPLFQVLFMPDVNLV 207
Db 122 DPPRLYLVLVITEGFREAVCTNTLHGMDKVTFGDAEVTRIPYPLMEMPDSRV 181
Qy 208 PDPEFHRSIGEFGVYPTPFNTGLCHLHDGCVTAAPMAVALVRNNTAVARGAAHLAFD 267
Db 182 ADPNCNHSRISGENFNPPLPFFTRPLRLFLFIAVGPBAVALRARNVDAVARAAHLAFD 241
Qy 268 ENHEGAVLPDPDTTYFOSSSGTTTARGAR 298
Db 242 ENHEGAALPADITTAFAASQG -KPGGAR 270

RESULT 7
US-10-237-551-230
; Sequence 230, Application US/10237551
; Publication No. US200301658201
; GENERAL INFORMATION:
; APPLICANT: Day, Craig H.
; APPLICANT: Parsons, Joseph M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
; TITLE REFERENCE: 210121..53C3
; CURRENT APPLICATION NUMBER: US/10/237,551
; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Herpes simplex virus
US-10-237-551-230

Query Match 8
Best Local Similarity 11.7%; Score 736; DB 14; Length 248;
Matches 139; Conservative 36; Mismatches 66; Indels 0; Gaps 0;
Qy 47 PLMENLTVEKTFSTSLAVSGARTGLAGAGITLKLTTSFESVFHHGGKHLVPLSSAA 106
Db 3 PLVGLTVSGFEANVAAVGSRTTGLGCTAVSLKMPHSYPSVIFHGGHLASTQA 62
Qy 107 PNLTACNAARERFGFSRCGPPDGAVENTGAEICTRIGLEPENTILYVYTALFKEAV 166
Db 63 PNLTLCERARRHGFSDYAPRCDLKHETGDALCERGLDSDRALYVITEGFEAV 122
Qy 167 FMCNVPLHNGGLDLYHNGDVRIPFQLMPDVNLVPDPENTHRSCEGFYPT 226
Db 123 CISNTFLHGGMDKVTFGIGDAEVTRIPYPLMMPDSRVIAFPNCNHSRISGENFNYPL 182
Qy 227 PFTNTGLCHLHDGCVTAAPMAVALVRNNTAVARGAAHLAFDENHEGAVLPDPDTTYFQS 286
Db 183 PFENRPLAKLFLFEAVGPAAVALRARNVDAVARAAHLAFDENHEGALPADEITTAFAEA 242
Qy 287 S 287

Db 243 S 243

RESULT 8
US-10-156-761-9121
; Sequence 9121, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HOBIKAWA, HIROSHI
; APPLICANT: SHIBA, TADATOSHI
; APPLICANT: SAKAKI, YOSHIOUKI
; APPLICANT: HATTORI, MASAHIRA
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO: 9121
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis

Query Match 9
Best Local Similarity 2.0%; Score 123,5; DB 14; Length 850;
Matches 182; Conservative 104; Mismatches 327; Indels 273; Gaps 37;
Qy 305 TSKPSPSGGFE-----RLASIMAAADTALHAEVIFNTGIVYEETPDIKEWPMFIGM 355
Db 3 TSRRTPPSAGLEPPSRPSPYRGRRAPAGQPADE-----DTGDTDETTAASADSPVGAGR 54
Qy 356 EGTPPR-----INALGUTSTARVAGVIGAMVFPDNAAKILTEVEDSGMTIE 399
Db 55 WGVRRTPTVRAKIVCLMMPVVSLLAWAY-----ATVSPAQDVARLROYQVQDVT 105
Qy 400 AKDGGGPSPSNRFYQFAGPHLAAMPQTDDGHLVSSQSTGSSNTSFSDYIAL---TCG 455
Db 106 RAPVAAAVALQARAAATRVIDPSAED---SGFTLAAAPDRAVDKLREGGHTYA 161
Qy 456 FGAPILLARLLFYLERCDAFTGCGHDALKYTFGTDFSEIPICSLCEKTRPVCAHTYHR 515
Db 162 DGADDAQVGRLETFVSGA-----BQURSLRG-----AVLER 194
Qy 516 IQRQMRERFGATRQPIGVFCTMN -SQYSDCDPILGNYAPYLIRKPGDOTEAAKATMOPD 573
Db 195 RARNDTEFGTYTRTAARFVGGLALTGIODAD-LGSDARVLL----EFSRAGEALAQED 248
Qy 574 YRATLRLFIDLEQPERL-LDRGAPCSEGSL-SVIVDHPFTERRLDTLRARIEQTITQFM 631
Db 249 AVLTSRRLAFTGDAVFTGAVDRLGTLR-----LSEREPAAAWQGVTGFA 302
Qy 670 FLVKRTHLAVYDIALSOCHCVF----YQQQVEGRNFNQFQFVLRREFD---LIFNG 720
Db 363 GLTPPPGAATLFGLAAVASLVLVSIYGRLVILISLNSALEIARRKLPOAMRKLRAG 422
Qy 721 GFISTSPSITYVLSSEGVSAP-NPTLGQDAPAGRFTFDGDLARVSVEIRDVKRNVRVFSG 779
Db 303 YADVRTAEDKVLANGPARIAAAQPAWDPAHARVOEGMRTIEADRGVADADPLTR 362
Qy 423 EBDYR-----AEAFGPAADETQVAAEALSTVRAAIAAVE----- 461
Qy 780 NCTNLSESEAARLVLGILASAQROEQKRDMLHGAFLKQFHGLLPRGMPPNSKSPNFO 839
Db 462 -----RAELASGISCV----- 472

Query 840 WFTWLLQRNOMPADKLTHEEITTTAAVYRFTTYYAAINFINLPPTCIGELAQFYMANLIL 899
 Database 473 -FVNLAIRSQI----LVRQLSLDSMERRSED-----PNEISDL--FRLDHLTT 515
 Query 900 KYCDHSOYLINTLTSITGAA--RRPRDPSSVLHWIRKDTSAAD---IETQ----- 945
 Database 516 RMRHAESEJL----ILSGAAGPGRAWRNPVSLSNVRAAVSEVEDYARVERQLPESAVV 570
 Query 946 AKALLEKTNPLPEWTTA -FTSTHLVRAAMNQRP-----MVVIGISISKYHGAGN 995
 Database 571 GAAVADLTILMAEVNAAQFSPPH-TRVRVTGEPNGYAVEVEDRGLGMKETLAEAN 629
 Query 996 NRVIQAGNWGLNGRNVPCLPFTDRTRFIIA-----CPRGGFICPVTGP 1041
 Database 630 RRIBQS-----EALDLESDRLGFFVSVRLAARHGKIVHLRTSPYGETTAVVLLP 679
 Query 1042 S----SGNRETT--LSDQYRGRIIVSGGANVQLIATYTVRAYCARA 1081
 Database 680 TALLHSGTAERVPRAADTGRD-ABPAYARVAASHOSVQQAVGRPA 724

RESULT 9
 US-10-454-351-34
 ; Sequence 34. Application US/10454351
 ; Publication No. US00010053301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Quark Biotech Inc.; Paz Einat, et al
 ; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS EXPRESSION PRODUCTS THERE
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: 010/FCT2-US2; EINAT,7E
 ; CURRENT APPLICATION NUMBER: US10/454,351
 ; CURRENT FILING DATE: 2003-06-14
 ; PRIOR APPLICATION NUMBER: US 09/991,630
 ; PRIOR FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: US 09/905,129
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 09/802,318
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: US 09/729,485
 ; PRIOR FILING DATE: 2000-12-04
 ; PRIOR FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 34
 ; LENGTH: 2597
 ; TYPE: PRT
 ; ORGANISM: Rattus rattus
 ; US-10-454-351-34

Query Match 2.0%; Score 123.5%; DB 12; Length 2597;
 Best Local Similarity 18.0%; Pred. No. 0.33%;
 Matches 145; Conservative 114; Mismatches 286; Indels 233; Gaps 40;

Query 416 AGPHLLANPQDF---RDGHVLSQSRTGSSN-----TEESVDYDALLCG 455
 Database 274 SGAFLLCTKPTIDPSLKSLSLTYQEDNSASTSPODFIEPPFGSLSLNMNTDLSGNKADMVCS 333

Query 456 FGAPILLARLFLYLERCDAGAFTGGHEDALVKTGTDFSEPCSLQBKHT-----CAHT 511
 Database 334 IOKP-----SRSTSPTAFFEENDYM--LNASTSNTLVCSVNDHICPvwQLLALYS 382

Query 512 TYHRLRQMP-----RFGQATRQPIGYFGTMNSOYSDCDP1GNY2APYLTLRKPGD 561

Database 383 DPLILLRKPOQTETPLSLRSRQLKQVRPDLIFTS-READY-ADPWFQOEKIVUQLNRT 441

Query 562 QTEAAAKTMQDTYRATLERFLDLEQERL-----LDR-----GAPCSSEG 601

Database 442 ATTLSLQIQUFSTDAQIALPRAEMRFLRYKWTMILMNPNPLERTVLGCCRITALSCPGKG 501

Query 602 -----LSSVIVDHPTR-----RILDALARIE OTTHQFMVU-----VETRD---- 639

Db 502 DPSPHLEWLLADGSKYRAPVUSEDGRILLDKNGKLELMQADSFDAGLYHCISTNDADADV 561
 Query 640 --YKIR--EGLSEATHSMALTFDPYSGAF---CPINFLVKRTHLAVYQDLAUSQCHV 691
 Database 562 LTYRIVTEPGEESTHDGVQHTVVTGFTEDLPLSTG-----VPDASIS--WI 608
 Query 692 FYGQOYEGRNFRNQFOQPVLRRFVDFLNGGFIISTRSTIVLSEGFSV--APNPT---- 743
 Database 609 LPGNTVFSQPSRDR -----QILANNTRLQQT -PKDQGHYQCTAANPSGADFSS 657
 Query 744 -----LGODAPAGTFTDGDALARSYEVIRDTRYKRNIVYFSGNCNTNLSEAARAR 791
 Database 658 FKVSYOKGQYRNVEHDEAGSGGLOB-PNSVSLQKOPASIK---LSASALTGSBAGKQ- 711
 Query 792 LVGLAZAYQROEKYRDMLHAGL-FILKQSHGLLFPRGMPPNPKSPNPQWFTLQ--R 847
 Database 712 ---VSGVHRKRNKHDLHRRRGDSTLRRRE--HRQQLSARRDQWQAALIEKAKK 765
 Query 848 NOMPADLTHBETT-----IAAVRKFEEYAAINFNFNLPPTOIGELAQFYMANLILK 900
 Database 766 NSVP---KROENTVYKPVPLAVPLVLTDEEKDASGMI--PP----- 802
 Query 901 YCDHSOYLINTLTSITGARRPRDPSSVLMWIKDVTSAADIEQAKALLEKTNJPELW 960
 Database 803 -DEEFNVLTKASGVPGRSPTADSPVNHGFMSTAAGTEVSTYATPQTLO-SEHLPDFK 859
 Query 961 TTAFTSTHYRAAM-----NORMVWLGTSISYKHGAGNRYFOAGNMG-- 1006
 Database 860 LFSVNTAVTKSMMPSIASKIEDTNTQNPLIIIFP-SVAEIRDSA-----QAGRASSQS 912
 Query 1007 --LNGGKNVCPBLFTFDRTRRFLIACPRGFB-----CPVYTG--PSSGN 1045
 Database 913 AHPVTCGNN---MATYGHNTYSSFTSKASTVLPQINPTSYGPQIPITGVSRPSSSD 966

RESULT 10
 US-10-206-576-358
 ; Sequence 358, Application US/10206576
 ; Publication No. US0001001749A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Choi et al
 ; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 ; NUMBER OF SEQUENCES: 497
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-R
 ; COMPUTER: Dell Latitude
 ; OPERATING SYSTEM: Windows 98
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/206,576
 ; FILING DATE: 29-Jul-2002
 ; CLASSIFICATION: Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/071,035
 ; FILING DATE: 1998-05-04
 ; APPLICATION NUMBER: US 60/046,655
 ; FILING DATE: 1997-05-16
 ; APPLICATION NUMBER: US 60/044,031
 ; FILING DATE: 1997-05-06
 ; APPLICATION NUMBER: US 60/066,009
 ; FILING DATE: 1997-11-14
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hyman, Mark J.
 ; REGISTRATION NUMBER: 46,789
 ; INFORMATION FOR SEQ ID NO: 358:
 ; INFORMATION FOR SEQ ID NO: 358:

SEQUENCE CHARACTERISTICS:		Qy	993 AGNNRVPQAGNWGLNGGKVNGLNGCPRGGFCICPTGPSSGNRETTLSD 1052
LENGTH: 1074 amino acids		Db	854 YENKYAFERGNE-----PVA-----KDAISLN 875
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: protein		Qy	1053 QVRGIIVSGAMVOLAATATVRAVAGR-----AGEMAFDWWLSLTDDDEFALRD 1102
SEQUENCE DESCRIPTION: SEQ ID NO: 358;		Db	876 QAQ-----TWNCTIERHVSITQTAHLLEDGSQTFTGSDVMDFDDSVTHYLD 923
US-10-206-577-358		Qy	1103 -EEELHDQIQTQLETPWTFVGEALBAVKILDE-----KTTAGD-----GBTPTNLAFFEF 1149
Query Match 2.0%; Score 123; DB 12; Length 1074;		Db	924 GSKEAFTFLYLIDFGTINKEIWKGKIEHEVNDKEFVTKVLAEKDTSKYPESTKEFE 982
Best Local Similarity 18.3%; Pred. No. 0.078;		Qy	1150 SCEPSHDTISNV-----LNISGSNISGSTPGLKRPEDDE 1185
Matches 206; Conservative 150; Mismatches 415; Indels 352; Gaps 52;		Db	983 -TEINYEKODGVNGKHINEDLKEKSQTLPKEVPTIPSPFKOPE 1024
Qy	250 RVNRNTAVYRGAHLAFADENHEGAVLPPDITYTYFQSSSGTTARGARRNDVNSTSCKPS 309		
Db	67 RTISLYAETNGAKOTVFC-IEPVSVIPIVTVHCV-----QKNPL 104		
		RESULT 11	
		US-10-206-576-394	
		; Sequence 394: Application US/10206576	
		; Publication No. US03001745A1	
		; GENERAL INFORMATION:	
		; APPLICANT: Choi et al.	
		; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides	
		; NUMBER OF SEQUENCES: 497	
		; CORRESPONDENCE ADDRESS:	
		; ADDRESS: Human Genome Sciences, Inc.	
		; STREET: 9410 Key West Avenue	
		; CITY: Rockville	
		; STATE: Maryland	
		; COUNTRY: USA	
		; ZIP: 20850	
		; COMPUTER READABLE FORM:	
		; MEDIUM TYPE: CD-R	
		; COMPUTER: Dell Latitude	
		; OPERATING SYSTEM: Windows 98	
		; SOFTWARE: ASCII Text	
		; CURRENT APPLICATION DATA:	
		; APPLICATION NUMBER: US/10/206,576	
		; FILING DATE: 29-Jul-2002	
		; PRIORITY APPLICATION DATA:	
		; APPLICATION NUMBER: US 09/071,035	
		; FILING DATE: 1998-05-04	
		; ATTORNEY/AGENT INFORMATION:	
		; NAME: Hyman, Mark J.	
		; REGISTRATION NUMBER: 46,789	
		; REFERENCE/DOCSET NUMBER: PB369R1D1	
		; INFORMATION FOR SEQ ID NO: 394:	
		; SEQUENCE CHARACTERISTICS:	
		; LENGTH: 1074 amino acids	
		; TYPE: amino acid	
		; STRANDEDNESS: single	
		; TOPOLOGY: linear	
		; MOLECULE TYPE: protein	
		; SEQUENCE DESCRIPTION: SEQ ID NO: 394:	
		US-10-206-576-394	
		Query Match 2.0%; Score 123; DB 12; Length 1074;	
		Best Local Similarity 18.3%; Pred. No. 0.078;	
		Matches 206; Conservative 150; Mismatches 415; Indels 352; Gaps 52;	
		Qy	250 RVRNTAVRGAHLAFADENHEGAVLPPDITYTYFQSSSGTTARGARRNDVNSTSCKPS 309
		Db	67 RTISLYAETNGAKOTVFC-IEPVSVIPIVTVHCV-----QKNPL 104
		Qy	310 PSGGFERRASIM-AADTALHAEVIFTNGTIVEE-----TPTDIKEWPMFI 353
		Db	105 PMSDKAKLVSVLWEKAGTDIDTMVMAQMVKMIEEVNGYKLHSIKRGGASVDIK 158
		Qy	354 GMEGTLPRLNALGSYTAR-----VAGVIG-AMVFSPENSAALYSTEVDGSGTNEAKDGGP 405
		Db	159 SIEBKINK-AIEBYQKPKSFHNTVTVKTLIGQSTTLDNKNEINLSEDKVQONTA 211
		Qy	406 GPSFMRFYCOAGPHALAANPQTDRDGHVLSQSSTGSSENTEFSYDYLALICGFGAPILLRL 465
		Db	212 ---NIDYRIVGNOLVLT-----NSNSKGTLTRKSAAGTGTP-VAYK 251
		Qy	466 FYLERCDAGAFTGCHGDALKYVTCGTFDSEIPCSLCEHTPRYCAGHTVHRQRXRFRFG 525
		Db	252 AGLQTVMAGALLKENTVAKINYETKGS-LKLKIDKEGSDCPDGNYA 304
		Qy	526 A-----TROPIQGVFTGTMNSQYSDCPDGNYA-----PYLLRKPGDOTEAAKATM 570
		Db	305 ALPSKDVDTDKDGTI-----SILDGIPGKTWTITERSVPDFWYIDTPMATTAKGETI 358
		Qy	571 QDTYRATLRLFIDLEQBLLDRGAPCSSEGLS-----SVIDHPTP-FRILDTRLA 621
		Db	359 SMTSKNMKRGQKQILLEKTGS-VEGTDLWDNTSLAGNTFAIRKDSPACEITVQEITDKEG 417
		Qy	622 RIBQTTQPMKVLYTETRYKIREGLSEATHSMALTEDP-----YSGAFCPTTNFLYKTR 675
		Db	418 RAB-TPKELANALELGTYVTE-TKSNNGFVTNTFKPTEKVELKYAQTVAUTSNVTKQ 473
		Qy	676 HLAIVQDIL-----SOCHCVFYGQQ-----EGRNERNHQFQPVLRRFVDL 717
		Db	474 NOETGETTILKEDXDTGENESOGKAETYLFTAKDQAVKWSAFK-----TEL 526
		Qy	718 FNGGPISRSITVTLSE-GPVSAPNPVQQ-----DAPAGTFPDGLARVSE 764
		Db	527 VKGETKASDDETVALDEKNOVAVKHLAINEYFWQETKAPEGTYLDETKYPSIKVYDNNE 586
		Qy	765 -----VTRDTRVQKVV-----FSGNTNLSEBAA-----PARLVGLASAYQROER 805
		Db	587 KNAVTRDVTAKQVIRGFDFEKKFAGSADGTAETGENDLSFKVSPLEGTXEITGAEDKA 646
		Qy	806 VDMHLGALGF-----LLKQFHGLLFPRGM-----PPNSKS- 838
		Db	647 TIANEQQLQFSDGJGKFENPYGDUILLEEA-----PEGFQKIPLEIRSTFKENDDYAKS 703
		Qy	839 QWFMTLQLRQN-----MPADKLTHREITTAAVKRTEEEAATNFNLP-PTCIGE 888
		Db	704 EYVTTIESQKQPKIJKMVTPYEXLTNNH-----FSVSLNRLMLDPEKEDSLTS 754
		Qy	889 LAQFYMANILJKYCDHSQQLINLUTSITGARRPRDPSSVLMWIKD-TVTSAAAD1ETQ 945
		Db	755 LATKDGNEKLINTDFTE-LVDKL-----RYNLHEIKEDWVVAQAIIDEA 799
		Qy	946 AKALLEKTNLPELMTTAATST-----HLVRAANNQRPVNVLGISISKYHGA 992
		Db	800 TKAQEKDKAKPVIVIAETTANKEKGTWKLHLKLTAE-----VLDLSIVLFNNY 853

105 PMSDKAKLUVSLVNEKAGTIDIDTNNAQKRNIIWEENNGYKLHSKIRLGASVDK----- 158
 354 GMEGLPLRNLALGSYTA-----VAGVIG-AMVPSPNSALYLTEVEDSGMTEAKDGGP 405
 Qy 159 SIEGKLINK-AIEEYQKPKPFHNTVKTILQSTLIDKELNTESEFDKVQNTA----- 211
 Db 406 GPSFRFQTAGPHIAANPQTDRDHVLSQSTGSSNTESFDYLAICFGAPLLARL 465
 Qy 212 ---NIDYRIVGNOLVLT-----NSNSKGTLKKSAGTGTP-VAYKK 251
 Db 466 FYLERDAGTTGAGTGGHDALXVTPGTFDSEPCSLSEKTRPVCAHTTVERLORMPRGO 525
 Qy 252 AGLOTMAGLDKPNTYAIIKINVTKGS-LKIKIDKESSDIVBETVFLU-----DGK 304
 Db 526 A-----TROPIGVFTMNNSQSDCDPLGNYA-----PYLILRKPGDQTEAAKATM 570
 Qy 305 ALPSRDUVTEDG-----SILDGPFGKTVTDEKSPDPMIDTPMANTKAGETI 358
 Db 571 QDTYRATLERLFIDLEQERLLDRGACPSSCGLS-----SIVIDDHPT---FRRILDTLRA 621
 Qy 359 SMTSKNQRQCKLRTG-VETGTDLWNDRYSLAGNTFAIRKDSPAGEBTVQEITTDKG 417
 Db 622 RIEQTTTOMYKLVETRDYKIREGLESBATHSMALTFDP-----YSGAFORBITINFLWKT 675
 Qy 418 RAE--TPKELANALELGTYYKTE--TKSSNGFVNTEFKPTKVELCYANOTVALTSNVKQO 473
 Db 676 HLAVVODLAL-----SQCHCVFYQQOV-----EGRNFRNQFPVPLRRRFVDL 717
 Qy 474 NOEITGETTLEKDKTGNEQSQGKAFKGKEYLETTAKDQAVKNSEAK-----TSL 526
 Db 718 ENGGFISTRISITVLSB-GPVSAAPNPTLQQ-----DAPAGRFTGDLAIVSVE----- 764
 Qy 527 VKGTKASDEVTLALDEKKNQAVKHLAINEFWQETKAPEGYTLDETKVSIIKVDNNE 586
 Db 765 ---VTDIYKTVRY-----FSGNCNTNLSEA-----RARLYGLASAYOREKR 805
 Qy 587 KNAVITDVTAKEQVTRFGDFEKFKAGSADGTAETSFNDJSFKVSPLEGKXETGAEDA 646
 Db 806 VDMHLGALGF-----LKKQFHGLLPRGM-----PPNSKS-----PNF 838
 Qy 647 TTACNEQLGFDGYKGPENLYGDDYLLFEEIA-----PGFOKITPLERSTFKENDYAKS 703
 Db 839 QWFWLQLQRNQ-----IMPADQKUTHEETIAAVKRFEEYAAINFNLPL--PTCIGE 888
 Qy 704 EYFTTIEEGQKOPIKNVTYKPEKLTNE-----FSYSLNLLMLDPEKDSLIS 754
 Db 889 LAOFYMANLILKYCDHSQYOLINTLTSITGARRPRDSETHWIRD-----VTSADDIETQ 945
 Qy 755 LATWDGKRNLTDFE-LVDKL-----RYNHIEKEDWYVQAQDVEA- 799
 Db 946 AYALLEKTEBNLPELWTAFTST-----HLVRALMNORMEMVYGIISIKYHGA 992
 Qy 800 TKAQEQDKEAKPVVIATASTANKERTGWKLHKLTAQ-----VLDKSVLFNTY 853
 Db 993 AGNNRVOQAGMNSLNGKKNVCPPLFTDRTRRFFIACPRGGFICPVGTPGSSGNRETTLS 1052
 Qy 854 YENKVAEAGNE-----PVA-----KDASLNN 875
 Db 1053 QTRGLIVSGAMVQLAYATVVRAGAR-----AQHMAFDWDWLSLTIDDEFIARDL----- 1102
 Qy 876 QQ-----TUNCTIERHVSQTKAHLEDGQTFHGVDNDMFDSVTHDVLJ 923
 Db 1103 -BELHDQIQTLETPTWVGEALEAVKILDE-----KTAGD-----GEPTPNLAFNFD 1149
 Qy 924 GSKEAFTILYALLPDGTNEKIMKSGKIEHEVNDKEFPTKTYLAEKVDTGKYPEGTKF----- 982
 Db 1150 SCFSPSHDTSNV-----LNISGSNTSGSTVPGLKRPEDDE 1185
 Qy 983 -TEINYERDGNVNGKHENDLKERSQTLTPEVPTIPSTPKQFB 1024
 Db 746 NTTOQAVGDTLTYTIAVQNTGNVPLTNEFQDAISSAVSFVANSVTINGVPQSGCLN----- 801

US-10-282-122A-45763 ; Sequence 45763, Application US/10282122A
 ; GENERAL INFORMATION:
 ; APPICANT: Wang, Liangguo
 ; APPICANT: Zamudio, Carlos
 ; APPICANT: Malone, Cheryl
 ; APPICANT: Haselbeck, Robert
 ; APPICANT: Olszen, Kari
 ; APPICANT: Zyskind, Judith
 ; APPICANT: Wall, Daniel
 ; APPICANT: Twick, John
 ; APPICANT: Carr, Grant
 ; APPICANT: Yamamoto, Robert
 ; APPICANT: Po-sych, R.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA 034A
 ; CURRENT APPLICATION NUMBER: US/10/282 122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NO: 7814
 ; SEQ ID NO: 45763
 ; LENGTH: 2358
 ; TYPE: PRT
 ; ORGANISM: Bacillus anthracis
 US-10-282-122A-45763
 Query Match 1.9%; Score 121; DB 12; Length 2358;
 Best Local Similarity 18.7%; Pred. No. 0; 5; Mismatches 517; Indels 464; Gaps 65;
 Matches 266; Conservative 178; Nmismatches 517; Entropy 153
 Db 575 SATFETPVEGQQPSGOATSNTVVTINADIIRTRKIVDRAFATVNDVLTYTWTIENTG 634
 Qy 57 TFTSSLAVYSGARTTGLAGAGITIKLTHFYSVYFHGGKHLPSAAAPNLTRACNA 116
 Db 520 TFWANSVINGVAPG-ANPASSINLGSINASQITVV--REFQVRVISNPLVNPINPA 574
 Qy 117 RERFSPRCG-PPVGD----AVBT- GAEICTRGLEP-----ENTI 153
 Db 154 LYLVVTAFLPKBAVMCNVPHYGGDITHNFGDVR PLFPYQLMFDPVNRLYPDPFNT 213
 Qy 635 NVLATNVVFQDPPIPQTTFI-TNSVYDGVSQPGANPATGFTVANISPGGSRVV-TFQV 691
 Db 214 HRSIGEGFVYPTPPNTGLCHLTHDCVIAPMVALVYRVN-----VITAVARGAAHLAFDE 268
 Db 692 RVTSPTSGGTIP----NRG-NVTANFVVIPTQNPPTINQRTNTVVTQNTGGLNVIKEY 745
 Qy 269 NHEGAVLPPDITYT-----YFQSSSS-----GTTARGARRDNVNSTSK 307
 Db 746 NTTOQAVGDTLTYTIAVQNTGNVPLTNEFQDAISSAVSFVANSVTINGVPQSGCLN----- 801

Qy 308 PSEGGPERLASMADAL-----HAEVIFN----TGYTEETPDIKEWPMF 352
 Db 802 -PNTGFS -LPNIPAAQTVVVTFDVLIIQDPNEDILQANTASQVNFS--BPPVT 854
 Qy 353 IGM-----EGTLPLNLNALGSYTAvgVIGAMVSPNSALYLTVEVDGMTEAKD 402
 Db 855 INPSNINNTVQGNFPEVKSVNTDVAGDVL-----VYTIEINAGSV--- 900
 Qy 403 GGPSPSFNFYQFQGP-----HLAANPQTDRGHVLSSOSTGSS---NT 443
 Db 901 ---PATNPNTQFSDPQGTLPFIENSVFYNGVLDQEGADFL--GFPNDLPGASVTVT 953
 Qy 444 EFTDYLALICGSPAPLLRFLIERDAGATGGHDALKVGTF--DSEIPOSIC 500
 Db 954 EVLIDEIPU-----GNNVYNSANVTGDFLVNTPEPPTVT 988
 Qy 501 EKHTRPVCQHHTVRLRQMPRFQCATR-----OPIGVFGTMQSQYSDCDPL 547
 Db 989 EPNTVM----TVVNSGUNIVIKVSATEAAGVGDITLYTTRIONGSQTAATTNVSELPIPS 1045
 Qy 548 GN--YAPYJILR-----KPGDQTEAKATMODTYATLERLFIDBEQRLLDGA-- 595
 Db 1046 GTTFVANSVTINGTPQPGNIPTCGFPLANIPVGMVTVAFQVTTSVPPNVLPNANVT 1105
 Qy 596 -----PCSESEGGLSSVIVDHP---TFRILDTLARIEOTTOFMKVLYTETR-- 638
 Db 1106 ADFOVSPLPPIPITVTSIVTRVNVGSSLNVMSKVNVLQAGVGDITL--YTILLONGT 1163
 Qy 639 -----DYKIREGLSEATHSMALT----FDPYSGAFCPTNFLYKRTLAVQDIA 684
 Db 1164 VPATNIIQFDPIPEGTAVANSTINGTVQGQADPMAG--FPVPTNIPGQTAVTFQ-- 1218
 Qy 685 LSQTHCVPVGQVQEGRNPNQFQ-----PVLRFFYDFTLNGPFISSTRSITVTL 732
 Db 1219 -----VTTTSIPEGGNTRNQSNITASFLINPANPPI----TTVNTNSNFTVNTQNTAQI 1267
 Qy 733 SEGVVSAPNPTLGDAPIRTF-----DGDILARVSVEVDIR----VGNRUVFSG 779
 Db 1268 NIQKTSV-----QQAALGETTYSVVRNNGTIVTATNSFIDPIAPETFYVANSITING 1322
 Qy 780 -----NCNTLSEAAARLVLGLASAYQ-----800
 Db 1323 TPDQGFDPNVGPFLNPIAGTSLTVFQTVIAPSTRGAVLNTASAATFLNPLQPPT 1382
 Qy 801 -----ROEKRVDMHNGALGELIKOFHGHLLFPRGMPPNSKSPNPFQW 840
 Db 1383 TTNSNTTVTTIPLPPGGEVTTATVDAAGA/GDVL-TYTTLISNYGIIPA----- 1434
 Qy 841 FWTLLQRNOMPADKLTHEITTAAVKRETFEEYAAINFLNPLPTCIGELAQFYMANILK 900
 Db 1435 -DVFQDQVPEGTPEVBSVTTGGVOQGLIN-PEIGTYTPLLACGSIETFOYTITE 1491
 Qy 901 YCDHSQYLNTLTSITGARRPDPSSV-----LHWIKRDVTSADD 941
 Db 1492 IPD-NEVILNDAVFTSQNPQEPPTETLNLVYVTTINTIAFVPPKLVDEKEVATVG 1550
 Qy 942 IETOQKALLEKTENLPELTTAFTSTHLVRAAMNQRPVVLGISISKYHGAAGNRNFQIA 1001
 Db 1551 ILTY-DVLLFNFGTVP-----ATVQYQDVLSSIAFEPSNTIDGVQLP 1594
 Qy 1002 G-----NWSGLNGGKNVCPPLFTFDRTREFITACPRGGFICP----- 1037
 Db 1595 GFNPANGFPLPDPINGEST--EVTFQVT---VVSVPNSNGTINTANTGFSV/LVPGEPVV 1649
 Qy 1038 -VTGPSSGNRBTTSQDQV9GILIVSGGAMYQLA1YATVYRAVGRACHMAFDWLSTJDE 1096
 Db 1650 IVTGESEN-----TTUTTVAER-----QFNVIKQVNRRAATLVGDVITYVQITNT-GT 1695
 Qy 1097 FLARDLEBHDQIQTLE-----TPWTEGCALEAVKILDEKTTAGDGETP----- 1141
 Qy 1696 VTANDV-----QFDITISAGASFVPSNTVINGALQ--TNLNPIITGFGDIPVGETVVT 1748
 Qy 1142 -----TNLAENFDSCPESHDDTSNVLN1SGSN1SGSTVPLKRP 1181

Db 1749 FQATVNTI-----PASGTITVNAVNITG--SCTLYVEG--EPP 1780
 Qy Sequence 2, Application US/09905129
 Db Patent No. US20020137705A1
 Qy GENERAL INFORMATION:
 Db APPLICANT: Binti, et al.
 Qy TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF
 Db TITLE OF INVENTION: AND USES THEREOF
 Db FILE REFERENCE: 540579-2
 Db CURRENT APPLICATION NUMBER: US/09/905,129
 Db PRIOR FILING DATE: 2001-07-13
 Db PRIOR APPLICATION NUMBER: 09/802,318
 Db PRIOR FILING DATE: 2001-01-08
 Db PRIOR APPLICATION NUMBER: 60/207,821
 Db PRIOR FILING DATE: 2000-05-30
 Db PRIOR APPLICATION NUMBER: 60/084,944
 Db PRIOR FILING DATE: 1998-05-11
 Db PRIOR APPLICATION NUMBER: 60/085,673
 Db PRIOR FILING DATE: 1998-05-15
 Db SOFTWARE: Patentin version 3.0
 Db SEQ ID NO: 2
 Db LENGTH: 2597
 Db TYPE: PRT
 Db ORGANISM: rattus species
 Db FEATURE:
 Db NAME/KEY: misc. feature
 Db LOCATION: (1)..(2597)
 Db OTHER INFORMATION: 'x' can be any amino acid
 Us-09-905-129-2

Query Match 1.9% Score 120.5; DB 9; Length 2597;
 Best Local Similarity 18.6%; Pred. No. 0.67%; Indels 233; Gaps 40;
 Matches 145; Conservative 113; Mismatches 287;

Qy 416 AGPHLANNPQTD-- RDGHVLSQSTQSGNTTE-----FSVDSLALICG 455
 Db 274 SGAFLCTKPTIDPSLKSKSLVTOEQDNGSASTSPQDFIEPFGSLSINTMXSGNKAADMVCS 333
 Qy 456 FGAPLARLFLYLERDAGAFTGGDKAKYVTFDIPSCSLOCERKTRPV---CAHT 511
 Db 334 1QKP-----SETSPTFTEENDYIM-LNNSPSTMVLCSYDYNH1QPVWQLLAJS 382
 Qy 512 TVHRLRQMRP-----RFGQTRQPIGVFGTMNSOYSDCDPGLGNTAPYLIRKPGD 561
 Db 383 DPLIIEKRQQLTEPSLSSRYKQVALREDIPISEADVR-APPFWQOEKIVLQART 441
 Qy 562 QTEAAKATMDTYATLERLFDIQLERL-----LDR-----GRAPSSEG 601
 Db 442 ATTLSLQLQIQFSTDQIALPRAEVRAERLKWTMILMNPKLERTVLYGGTIAISPGKG 501
 Qy 602 -----LSSVYUDHPPR-----RILDILTRARIE-QTTTOENKVL---VETD----- 639
 Db 502 DPSPHLWLLADGSKRAPVYSEDRILIDRKGLELQADSFAGLYHCISTNDADADV 561
 Qy 640 -YKIR -EGISEAETHSMALTEDPYSGAF---CPIITNEFLVKSTHLLAVYDLSLQCHCV 691
 Db 562 LTYRATTVBPGESTDSGQHTVYGETIDLPCUSTG-----VTDASIS---WI 608
 Qy 692 FYQQQVEGRNFRNQFQPVULRRFVDFLNGCFISTRISITVTLSEGPV -- APNPT ----- 743
 Db 609 LPGNTVFSOPERDR-----QILNGNTLRLQVT-PKDQGHYOCYBAANPSGADFSS 657
 Qy 744 -----LGQDAPASRTFDEDARYSVEVIRVKNRUVFSGNNTNLSEARAR 791
 Db 658 FKUSVOKKGQRMVBEREAGGSLGE -PNSVSVSLKQPA5LK-----LSA-SALTGEAGKQ- 711
 Qy 792 LVGLASAYOREKRYVDMHLHGALG-FLKQFHGLLFRGRMPNSKSPPNPWFWTLIQ--R 847
 Qy

RESULT 14
US-09-905-129-10
; Sequence 10, Application US/09905129
; Patent No. US2002137705A1
; GENERAL INFORMATION:
; APPLICANT: Binat, et al.
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 540579-2007.2
; CURRENT APPLICATION NUMBER: US/09/905,129
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/802,318
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/207,821
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/084,944
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: 60/085,673
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 10
; LENGTH: 2597
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2597)
; OTHER INFORMATION: 'x' can be any amino acid
US -09-905-129-10

Query Match Score 120.5; DB 9; Length 2597;
Best Local Similarity 18.6%; Pred. No. 0.67%; Mismatches 113; Gaps 40;
Matches 145;

Qy 416 AGPHLAANPQTD--RDGHVILSSQSTGSSNTE-----FSDYLAJCG 455
Db 274 SGAFICLKTPIDPSLKSRSILVTQDNGSASTSPODFIPFGSISLNNTXXSNTKADIVCS 333
Qy 456 FGAPILLRFLYLERCDAGFTGGHDAKYVGTGPDESEPCSLCEKTRPV--CAHT 511
Db 334 IQKP-----SRTSPTAFTENDYM-LNVSFSTNLVCSVDYHNIQPYWOLLALYS 382
Qy 512 TVHR.RORM-----RFGQATRQTFPSLSSRYKVALPEDIIFTSIAADR-ADPFNWQEKIVQLNRT 441
Db 383 DSPLILERKEQLETFPSLSSRYKVALPEDIIFTSIAADR-ADPFNWQEKIVQLNRT 441
Qy 562 QTEAAKATMDTYRATLERFLFIDEQERL-----LDR-----GAPCSSEG 601
Db 442 ATTGSTLQIQTSDQIAFRFAERAKWTHMLMMNNPKRLTFLVGGTTIALSCPGK 501
Qy 602 ----LSSVIVDHPPTFR-----RILDTLRAIE-QTTQFMKVLF--VETRD-----639
Db 502 DPPSHLEWLADGSKVAPYVSEDRILIDNGKLEONADSFDAGLYHCISTNDADAV 561

RESULT 15
US-09-905-129-13
; Sequence 13, Application US/09905129
; Patent No. US2002137705A1
; GENERAL INFORMATION:
; APPLICANT: Binat, et al.
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 540579-2007.2
; CURRENT APPLICATION NUMBER: US/09/905,129
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/802,318
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/207,821
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/084,944
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/802,318
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/207,821
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/084,944
; SEQ ID NO: 13
; LENGTH: 2597
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2597)
; OTHER INFORMATION: 'x' can be any amino acid
US -09-905-129-13

Query Match Score 120.5; DB 9; Length 2597;
Best Local Similarity 18.6%; Pred. No. 0.67%; Mismatches 113; Gaps 40;
Matches 145;

Qy 416 AGPHLAANPQTD--RDGHVILSSQSTGSSNTE-----FSDYLAJCG 455
Db 274 SGAFICLKTPIDPSLKSRSILVTQDNGSASTSPODFIPFGSISLNNTXXSNTKADIVCS 333
Qy 456 FGAPILLRFLYLERCDAGFTGGHDAKYVGTGPDESEPCSLCEKTRPV--CAHT 511
Db 334 IQKP-----SRTSPTAFTENDYM-LNVSFSTNLVCSVDYHNIQPYWOLLALYS 382
Qy 512 TVHR.RORM-----RFGQATRQTFPSLSSRYKVALPEDIIFTSIAADR-ADPFNWQEKIVQLNRT 441
Db 383 DSPLILERKEQLETFPSLSSRYKVALPEDIIFTSIAADR-ADPFNWQEKIVQLNRT 441
Qy 562 QTEAAKATMDTYRATLERFLFIDEQERL-----LDR-----GAPCSSEG 601
Db 442 ATTGSTLQIQTSDQIAFRFAERAKWTHMLMMNNPKRLTFLVGGTTIALSCPGK 501
Qy 602 ----LSSVIVDHPPTFR-----RILDTLRAIE-QTTQFMKVLF--VETRD-----639
Db 274 SGAFICLKTPIDPSLKSRSILVTQDNGSASTSPQDFIEPPGSLSLNMXTXSGNKADMVCs 333

Qy 456 FGAPILLARILLYLERDAGAFTGGHDALCKVUTGTFDSEIPCSLOCXKHTTPV---CAHT 511
 Db 334 IQKP-----SRTSPTAEEENDYIM-LNASFSTNIVCSVDYNHICPWNOLLALYS 382
 Qy 512 TVERLORMP-----REFQATRQPQGVFGTMNSQSDCPLGNAYAPYLILRKPD 561
 Db 383 DSSLTLEKPKQTETPSLSQYKVALRPEDIESTEADYR-ADPEWFOCEKIVOLART 441
 Qy 562 QTEAAKATMODYTATLERLFDIDEERL-----LDR-----GAPCSSSG 601
 Db 442 ATTLSLQIQFSTDQIALPRAEMAEERLKTMLMANNPKLERTVLYGGTTIALSCPGK 501
 Qy 602 -----LSSVIVDHPPTFR-----RILDTLURARIE-QTTTQFMKV-----VETRD---- 639
 Db 502 DPSHIELWLADGSKTYKRAPYVSEDRGRLIDKNGKEJLQMDSDFDGLYRISTNDADAV 561
 Qy 640 --YKIR--EGLSEATHSMALTFDPYSGAF----CPITNFLYKTRTHLAVYODLALSQCHCV 691
 Db 562 LTYRIVTEPYCESTSDGCVHSTVVGETDLPCUSTG-----VEDASLS--WI 608
 Qy 692 PYQQVEGRNPRNQFQBVLRRFVDLFNGGPISTRISITVSEGTVS-APNPT---- 743
 Db 609 LPNTNTFSQPSDR-----QINLNNGTILRILQVT-PDQDGHQYCVAANPSGADESS 657
 Qy 744 -----LGQDAPAGRTFDGDIARYSVEVDIRKVNRRVVFSGNTNLSEARR 791
 Db 658 FKVSVQKGQVMVEHDEAGGSLGLB-EANSVSVSLKOPASIK---LSASALTGEAGKQ- 711
 Qy 792 LVGLASAYQRQEKRVDMLHGALG-FLIKOFHGLLPRGMPPNSKSPNPONFWTLIQ--R 847
 Db 712 ---VSGYHRKVKHDLIIRRQLRGDTSLLRFP--HRRQLPLSARRIDQFWAALEKACK 765
 Qy 848 NOMPADKLTHEITT-----IAAYKRTRFREYAAINFINLPPTCTIGELAQFYMANLILK 900
 Db 766 NSVP---KQDNTTVPVPLAVPLVLTDEKDASGM-PP----- 802
 Qy 901 YDHSQYLVINTLTSITTGARRPRDPSSVLLHWRKDVTSAADIEQTAKALLEKTELPELW 960
 Db 803 -DEEFNVLKTKTASGVGRSPADSGEVNHFMTSASGPSTVSYNPTQI-Q-SEHLPDFK 859
 Qy 961 TTAFSTPHLVRAM-----NQRMVYVLGISISKCHGAAGNNRVOAGNWSG- 1006
 Db 860 LFSVNTNGTAVTKSMNPSTASKIEDDTNQNPTIIFP-SVAETRDSA-----QAGRASSQS 912
 Qy 1007 ---LNGGKNCPLFPTDRTTRILLACRGFT-----CPVTG---PSSGN 1045
 Db 913 AHPVTGGN---MATYGHNTYSSFSKASTVLLQPINPTESYGPQIPITVSRPSSSD 966

RESULT 16
 US-09-991-630-2
 Sequence 2, Application US/09991630
 Patent No. US20020151514A1
 GENERAL INFORMATION:
 APPLICANT: Einat, et al
 TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS EXPRESSION PRODUCTS THEREOF
 FILE REFERENCE: 540579-007.J
 CURRENT APPLICATION NUMBER: US/09/991,630
 CURRENT FILING DATE: 2001-11-06
 PRIOR APPLICATION NUMBER: 09/905,129
 PRIOR FILING DATE: 2001-07-09
 PRIORITY NUMBER: 09/802,318
 PRIOR FILING DATE: 2001-03-08
 PRIORITY NUMBER: 09/729,485
 PRIOR FILING DATE: 2000-12-04
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: Patent in version 3.0
 LENGTH: 2597
 SEQ ID NO 2
 TYPE: PRT
 ORGANISM: Rattus species
 FEATURE:

; NAME/KEY: misc feature
; LOCATION: (1)-(297)
; OTHER INFORMATION: 'x' can be any amino acid
; US-09-991-630-2
Query Match 1.9%; Score 120.5%; DB 9; Length: 2597;
Best Local Similarity 18.6%; Pred. No. 0.67%; Indels 233; Gaps 40;
Matches 145; Conservative 113; Mismatches 287; ;
416 AGPHLAANPQTD--RIGHVLUSSQSTQSTSSNTE----PSYDYLALIG 455
Db 274 SGAFLCKRKPTIDPSLKSKSLVTOEDNOSSAATSPQDFTEPFGSLSLNNTXXSGNKADMVC 333
Qy 456 FGAPILLARILLYLERDAGAFTGGHDALCKVUTGTFSEIPSLCERHTRPV---CAHT 511
Db 334 IQKP-----SRTSPTAEEENDYIM-LNASFSTNIVCSVDYHICPWNOLLALYS 382
Qy 512 TVERLORMP-----REFQATRQPQGVFGTMNSQSDCPLGNAYAPYLILRKPD 561
Db 383 DSSLTLEKPKQTETPSLSQYKVALRPEDIESTEADYR-ADPEWFOCEKIVOLART 441
Qy 562 OTEAAKATMODYTATLERLFDIDEERL-----LDR-----GAPCSSEG 601
Db 442 ATTLSLQIQFSTDQIALPRAEMARLKTWNLMMNNPKLERTVLYGGTTIALSCPGK 501
Qy 512 TVERLORMP-----REFQATRQPQGVFGTMNSQSDCPLGNAYAPYLILRKPD 561
Db 383 DPSHIELWLADGSKTYKRAPYVSEDRGRLIDKNGKLEQMADESFAGLYHC1STNDADAV 561
Qy 602 -----LSSVIVDPTFR-----RILDTLURARIE-QTTTQFMVU-----VETRD---- 639
Db 502 DPSHIELWLADGSKTYKRAPYVSEDRGRLIDKNGKLEQMADESFAGLYHC1STNDADAV 561
Qy 640 --YKIR--EGLSEATHSMALTFDPYSAF---CPTTNFLYKTRTHLAVQDIALSQCHCV 691
Db 662 LYTRIVTEPYCESTSDGCVHSTVVGETDLPCUSTG-----VPRBASIS--WI 608
Qy 692 FYGQQVEGRNPRNQFQPVLRRFVDLFNGGPISTRISITVSEGTVS-APNPT---- 743
Db 609 LPGNTVFSQPSDR-----QINLNNGTILRILQVT-PDQGHYQCVAAANPSGADESS 657
Qy 744 -----LGQDAPAGRTFDGDIARYSVEVDIRKVNRRVVFSGNTNLSEARR 791
Db 658 EKVSVQKGQVMVEHDEAGGSLGLB-EANSVSVSLKOPASIK---LSASALTGEAGKQ- 711
Qy 792 LVGLASAYQRQEKRVDMLHGALG-FLIKOFHGLLPRGMPPNSKSPNPONFWTLIQ--R 847
Db 712 ---VSGYHRKVKHDLIIRRQLRGDTSLLRFP--HRRQLPLSARRIDQFWAALEKACK 765
Qy 848 NOMPADKLTHEITT-----IAAYKRTRFREYAAINFINLPPTCTIGELAQFYMANLILK 900
Db 766 NSVP---KQDNTTVPVPLAVPLVLTDEKDASGM-PP----- 802
Qy 901 YDHSQYLVINTLTSITTGARRPRDPSSVLLHWRKDVTSAADIEQTAKALLEKTELPELW 960
Db 803 -DEEFNVLKTKTASGVGRSPADSGEVNHFMTSASGPSTVSYNPTQI-Q-SEHLPDFK 859
Qy 961 TTAFSTPHLVRAM-----NQRMVYVLGISISKCHGAAGNNRVOAGNWSG- 1006
Db 860 LFSVNTNGTAVTKSMNPSTASKIEDDTNQNPTIIFP-SVAETRDSA-----QAGRASSQS 912
Qy 1007 ---LNGGKNCPLFPTDRTTRILLACRGFT-----CPVTG---PSSGN 1045
Db 913 AHPVTGGN---MATYGHNTYSSFSKASTVLLQPINPTESYGPQIPITVSRPSSSD 966

RESULT 17
US-09-991-630-10
Sequence 10, Application US/09991630
Patent No. US20020151514A1
GENERAL INFORMATION:
APPLICANT: Einat, et al
TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS EXPRESSION PRODUCTS THEREOF
FILE REFERENCE: 540579-007.J
CURRENT APPLICATION NUMBER: US/09/991,630
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 09/905,129
PRIOR FILING DATE: 2001-07-09
PRIORITY NUMBER: 09/802,318
PRIOR FILING DATE: 2001-03-08
PRIORITY NUMBER: 09/729,485
PRIOR FILING DATE: 2000-12-04
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent in version 3.0
LENGTH: 2597
SEQ ID NO 2
TYPE: PRT
ORGANISM: Rattus species
FEATURE:

```

RESULT 18
US-09-991-630-13
; Sequence 13, Application US/09991630
; Patent No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: Einat, et al
; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF
; FILE REFERENCE: 544579-2007.3
; CURRENT APPLICATION NUMBER: US/09/991-630
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/905,129
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/802,318
; PRIOR FILING DATE: 2000-12-04
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO: 10
; LENGTH: 2597
; ORGANISM: Rattus species
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1..(2597)
; OTHER INFORMATION: 'x' can be any amino acid

 416 AGPHIAANQTD--RDGVVLSSGSTGSANTE-----PSVDYLALIGC 455
 274 SGAFIICTKTIDPFLKSQSLVTQEDNGSASTSPDFFIEFGSLSLNNTXXSGNKADMVCS 333
 456 FGAPLLARILFYLERCDAGAFTGGHGDALKYVTCFSDSIPSCSCLCERTRPV---CAHT 511
 334 IQKP-----SRTSPFAFEENDYIM-LNASFSTNLVCSVDYNHQPWQLLALYS 382
 512 TVHLRLRQMP-----RFGQATRQTCIGVFTCMNSQYSDCDPLGNAYAPIYLRLKEQD 561
 383 DSPLILERPQLTBTPLSSRYKQVALDRAFTSIEADVR-ADPFWFQEQKIVLQLNRT 441
 29 YQ
 562 QTEAAKATMQDTYRATLERLFIDEQERL-----LDR-----GAPCSSEG 601
 442 ATTLSLTLQQFSTAQIALPRAENRAERLKWTMILLMMNNPKLERTVLYCGTIALSCPERKG 501
 602 -----LSSYTVDHPTFR-----RILDTLRARLE-QTTQFMKV-----VERD---- 639
 502 DPSPHLEWLADGSKVRAPYVSEDRILLDKNGKLEQMLADSFDAGLYCISTNDADAV 561
 640 --YKTR--EGLSEATHSMALTFDPGSAF----CPITNFVLRKRTHLAVVQDIALSOCHIV 691
 562 LTYRITVVEYGETHDGVQHTVVGETIDLPLCLSTG-----VPDASITS--WI 608
 692 FYGQOVEGHNFRNQFQPVLRRFYDLENGFISTRSTVTLSEGPS--APNPT---- 743
 603 LPGNTVVFSSPSRDR-----QILNQTLRLIQVT-PKDQHYOCVAANPGADEFS 657
 744 -----LGDDAPASRTFDDDLARYSVEVTRDIVRTRVPPSGCTNLSEAAAR 791
 658 FKVSVQKGKQRMVEDREAGGSGLGE -PNSVSVLKQPAISK---LSA8ALTSEAGKQ- 711
 792 LVGLASAYQKERRQEYRDMILHGALG-FLLKOPHGLIPRGMNPNSKSPNPWFVTLQ---R 847
 712 ---VSGVHAKRNKHDLIIRRGRDSTLRLRPRE-HRRQDLSARRIDPQWAALEKAKK 765
 848 NQMPADKLTHEETI-----IAVVKRFTEEYAAAINFINLPPTCIGELAQFYMANLILK 900
 766 NSVP---KQEQNTTVKPVVLAVPIVLTDEKDASGM--PP----- 802
 901 YCDHSQYLINTLTSITGARRPRDSSVLMIRDVTSADIEOKALLEKTNLPELW 960
 803 ---DERFMVLLTKASGYGPGRSPTADSGPVNNGEMTSIASGTEVSYNPOTQ-SHLLPDK 859
 961 TTAFTSTHLYRAM-----NORMPKVLLISXKRGAGNNKVFOAGMSG-- 1006
 860 LFSVNTGATVSKMPSIASKIEDTINQNPPIIFP-SVAFIRDSA---QAGRASSQS 912
 1007 ---LNGKKNVCPLEFDTRRFFIACPRGGFI-----CPVYG---PSSGN 1045
 29 YQ
 30 DDB
 31 DDB
 32 DDB
 33 DDB
 34 DDB
 35 DDB
 36 DDB
 37 DDB
 38 DDB
 39 DDB
 40 DDB
 41 DDB
 42 DDB
 43 DDB
 44 DDB
 45 DDB
 46 DDB
 47 DDB
 48 DDB
 49 DDB
 50 DDB
 51 DDB
 52 DDB
 53 DDB
 54 DDB
 55 DDB
 56 DDB
 57 DDB
 58 DDB
 59 DDB
 60 DDB
 61 DDB
 62 DDB
 63 DDB
 64 DDB
 65 DDB
 66 DDB
 67 DDB
 68 DDB
 69 DDB
 70 DDB
 71 DDB
 72 DDB
 73 DDB
 74 DDB
 75 DDB
 76 DDB
 77 DDB
 78 DDB
 79 DDB
 80 DDB
 81 DDB
 82 DDB
 83 DDB
 84 DDB
 85 DDB
 86 DDB
 87 DDB
 88 DDB
 89 DDB
 90 DDB
 91 DDB
 92 DDB
 93 DDB
 94 DDB
 95 DDB
 96 DDB
 97 DDB
 98 DDB
 99 DDB
 100 DDB
 101 DDB
 102 DDB
 103 DDB
 104 DDB
 105 DDB
 106 DDB
 107 DDB
 108 DDB
 109 DDB
 110 DDB
 111 DDB
 112 DDB
 113 DDB
 114 DDB
 115 DDB
 116 DDB
 117 DDB
 118 DDB
 119 DDB
 120 DDB
 121 DDB
 122 DDB
 123 DDB
 124 DDB
 125 DDB
 126 DDB
 127 DDB
 128 DDB
 129 DDB
 130 DDB
 131 DDB
 132 DDB
 133 DDB
 134 DDB
 135 DDB
 136 DDB
 137 DDB
 138 DDB
 139 DDB
 140 DDB
 141 DDB
 142 DDB
 143 DDB
 144 DDB
 145 DDB
 146 DDB
 147 DDB
 148 DDB
 149 DDB
 150 DDB
 151 DDB
 152 DDB
 153 DDB
 154 DDB
 155 DDB
 156 DDB
 157 DDB
 158 DDB
 159 DDB
 160 DDB
 161 DDB
 162 DDB
 163 DDB
 164 DDB
 165 DDB
 166 DDB
 167 DDB
 168 DDB
 169 DDB
 170 DDB
 171 DDB
 172 DDB
 173 DDB
 174 DDB
 175 DDB
 176 DDB
 177 DDB
 178 DDB
 179 DDB
 180 DDB
 181 DDB
 182 DDB
 183 DDB
 184 DDB
 185 DDB
 186 DDB
 187 DDB
 188 DDB
 189 DDB
 190 DDB
 191 DDB
 192 DDB
 193 DDB
 194 DDB
 195 DDB
 196 DDB
 197 DDB
 198 DDB
 199 DDB
 200 DDB
 201 DDB
 202 DDB
 203 DDB
 204 DDB
 205 DDB
 206 DDB
 207 DDB
 208 DDB
 209 DDB
 210 DDB
 211 DDB
 212 DDB
 213 DDB
 214 DDB
 215 DDB
 216 DDB
 217 DDB
 218 DDB
 219 DDB
 220 DDB
 221 DDB
 222 DDB
 223 DDB
 224 DDB
 225 DDB
 226 DDB
 227 DDB
 228 DDB
 229 DDB
 230 DDB
 231 DDB
 232 DDB
 233 DDB
 234 DDB
 235 DDB
 236 DDB
 237 DDB
 238 DDB
 239 DDB
 240 DDB
 241 DDB
 242 DDB
 243 DDB
 244 DDB
 245 DDB
 246 DDB
 247 DDB
 248 DDB
 249 DDB
 250 DDB
 251 DDB
 252 DDB
 253 DDB
 254 DDB
 255 DDB
 256 DDB
 257 DDB
 258 DDB
 259 DDB
 260 DDB
 261 DDB
 262 DDB
 263 DDB
 264 DDB
 265 DDB
 266 DDB
 267 DDB
 268 DDB
 269 DDB
 270 DDB
 271 DDB
 272 DDB
 273 DDB
 274 DDB
 275 DDB
 276 DDB
 277 DDB
 278 DDB
 279 DDB
 280 DDB
 281 DDB
 282 DDB
 283 DDB
 284 DDB
 285 DDB
 286 DDB
 287 DDB
 288 DDB
 289 DDB
 290 DDB
 291 DDB
 292 DDB
 293 DDB
 294 DDB
 295 DDB
 296 DDB
 297 DDB
 298 DDB
 299 DDB
 300 DDB
 301 DDB
 302 DDB
 303 DDB
 304 DDB
 305 DDB
 306 DDB
 307 DDB
 308 DDB
 309 DDB
 310 DDB
 311 DDB
 312 DDB
 313 DDB
 314 DDB
 315 DDB
 316 DDB
 317 DDB
 318 DDB
 319 DDB
 320 DDB
 321 DDB
 322 DDB
 323 DDB
 324 DDB
 325 DDB
 326 DDB
 327 DDB
 328 DDB
 329 DDB
 330 DDB
 331 DDB
 332 DDB
 333 DDB
 334 DDB
 335 DDB
 336 DDB
 337 DDB
 338 DDB
 339 DDB
 340 DDB
 341 DDB
 342 DDB
 343 DDB
 344 DDB
 345 DDB
 346 DDB
 347 DDB
 348 DDB
 349 DDB
 350 DDB
 351 DDB
 352 DDB
 353 DDB
 354 DDB
 355 DDB
 356 DDB
 357 DDB
 358 DDB
 359 DDB
 360 DDB
 361 DDB
 362 DDB
 363 DDB
 364 DDB
 365 DDB
 366 DDB
 367 DDB
 368 DDB
 369 DDB
 370 DDB
 371 DDB
 372 DDB
 373 DDB
 374 DDB
 375 DDB
 376 DDB
 377 DDB
 378 DDB
 379 DDB
 380 DDB
 381 DDB
 382 DDB
 383 DDB
 384 DDB
 385 DDB
 386 DDB
 387 DDB
 388 DDB
 389 DDB
 390 DDB
 391 DDB
 392 DDB
 393 DDB
 394 DDB
 395 DDB
 396 DDB
 397 DDB
 398 DDB
 399 DDB
 400 DDB
 401 DDB
 402 DDB
 403 DDB
 404 DDB
 405 DDB
 406 DDB
 407 DDB
 408 DDB
 409 DDB
 410 DDB
 411 DDB
 412 DDB
 413 DDB
 414 DDB
 415 DDB
 416 DDB
 417 DDB
 418 DDB
 419 DDB
 420 DDB
 421 DDB
 422 DDB
 423 DDB
 424 DDB
 425 DDB
 426 DDB
 427 DDB
 428 DDB
 429 DDB
 430 DDB
 431 DDB
 432 DDB
 433 DDB
 434 DDB
 435 DDB
 436 DDB
 437 DDB
 438 DDB
 439 DDB
 440 DDB
 441 DDB
 442 DDB
 443 DDB
 444 DDB
 445 DDB
 446 DDB
 447 DDB
 448 DDB
 449 DDB
 450 DDB
 451 DDB
 452 DDB
 453 DDB
 454 DDB
 455 DDB
 456 DDB
 457 DDB
 458 DDB
 459 DDB
 460 DDB
 461 DDB
 462 DDB
 463 DDB
 464 DDB
 465 DDB
 466 DDB
 467 DDB
 468 DDB
 469 DDB
 470 DDB
 471 DDB
 472 DDB
 473 DDB
 474 DDB
 475 DDB
 476 DDB
 477 DDB
 478 DDB
 479 DDB
 480 DDB
 481 DDB
 482 DDB
 483 DDB
 484 DDB
 485 DDB
 486 DDB
 487 DDB
 488 DDB
 489 DDB
 490 DDB
 491 DDB
 492 DDB
 493 DDB
 494 DDB
 495 DDB
 496 DDB
 497 DDB
 498 DDB
 499 DDB
 500 DDB
 501 DDB
 502 DDB
 503 DDB
 504 DDB
 505 DDB
 506 DDB
 507 DDB
 508 DDB
 509 DDB
 510 DDB
 511 DDB
 512 DDB
 513 DDB
 514 DDB
 515 DDB
 516 DDB
 517 DDB
 518 DDB
 519 DDB
 520 DDB
 521 DDB
 522 DDB
 523 DDB
 524 DDB
 525 DDB
 526 DDB
 527 DDB
 528 DDB
 529 DDB
 530 DDB
 531 DDB
 532 DDB
 533 DDB
 534 DDB
 535 DDB
 536 DDB
 537 DDB
 538 DDB
 539 DDB
 540 DDB
 541 DDB
 542 DDB
 543 DDB
 544 DDB
 545 DDB
 546 DDB
 547 DDB
 548 DDB
 549 DDB
 550 DDB
 551 DDB
 552 DDB
 553 DDB
 554 DDB
 555 DDB
 556 DDB
 557 DDB
 558 DDB
 559 DDB
 560 DDB
 561 DDB
 562 DDB
 563 DDB
 564 DDB
 565 DDB
 566 DDB
 567 DDB
 568 DDB
 569 DDB
 570 DDB
 571 DDB
 572 DDB
 573 DDB
 574 DDB
 575 DDB
 576 DDB
 577 DDB
 578 DDB
 579 DDB
 580 DDB
 581 DDB
 582 DDB
 583 DDB
 584 DDB
 585 DDB
 586 DDB
 587 DDB
 588 DDB
 589 DDB
 590 DDB
 591 DDB
 592 DDB
 593 DDB
 594 DDB
 595 DDB
 596 DDB
 597 DDB
 598 DDB
 599 DDB
 600 DDB
 601 DDB
 602 DDB
 603 DDB
 604 DDB
 605 DDB
 606 DDB
 607 DDB
 608 DDB
 609 DDB
 610 DDB
 611 DDB
 612 DDB
 613 DDB
 614 DDB
 615 DDB
 616 DDB
 617 DDB
 618 DDB
 619 DDB
 620 DDB
 621 DDB
 622 DDB
 623 DDB
 624 DDB
 625 DDB
 626 DDB
 627 DDB
 628 DDB
 629 DDB
 630 DDB
 631 DDB
 632 DDB
 633 DDB
 634 DDB
 635 DDB
 636 DDB
 637 DDB
 638 DDB
 639 DDB
 640 DDB
 641 DDB
 642 DDB
 643 DDB
 644 DDB
 645 DDB
 646 DDB
 647 DDB
 648 DDB
 649 DDB
 650 DDB
 651 DDB
 652 DDB
 653 DDB
 654 DDB
 655 DDB
 656 DDB
 657 DDB
 658 DDB
 659 DDB
 660 DDB
 661 DDB
 662 DDB
 663 DDB
 664 DDB
 665 DDB
 666 DDB
 667 DDB
 668 DDB
 669 DDB
 670 DDB
 671 DDB
 672 DDB
 673 DDB
 674 DDB
 675 DDB
 676 DDB
 677 DDB
 678 DDB
 679 DDB
 680 DDB
 681 DDB
 682 DDB
 683 DDB
 684 DDB
 685 DDB
 686 DDB
 687 DDB
 688 DDB
 689 DDB
 690 DDB
 691 DDB
 692 DDB
 693 DDB
 694 DDB
 695 DDB
 696 DDB
 697 DDB
 698 DDB
 699 DDB
 700 DDB
 701 DDB
 702 DDB
 703 DDB
 704 DDB
 705 DDB
 706 DDB
 707 DDB
 708 DDB
 709 DDB
 710 DDB
 711 DDB
 712 DDB
 713 DDB
 714 DDB
 715 DDB
 716 DDB
 717 DDB
 718 DDB
 719 DDB
 720 DDB
 721 DDB
 722 DDB
 723 DDB
 724 DDB
 725 DDB
 726 DDB
 727 DDB
 728 DDB
 729 DDB
 730 DDB
 731 DDB
 732 DDB
 733 DDB
 734 DDB
 735 DDB
 736 DDB
 737 DDB
 738 DDB
 739 DDB
 740 DDB
 741 DDB
 742 DDB
 743 DDB
 744 DDB
 745 DDB
 746 DDB
 747 DDB
 748 DDB
 749 DDB
 750 DDB
 751 DDB
 752 DDB
 753 DDB
 754 DDB
 755 DDB
 756 DDB
 757 DDB
 758 DDB
 759 DDB
 760 DDB
 761 DDB
 762 DDB
 763 DDB
 764 DDB
 765 DDB
 766 DDB
 767 DDB
 768 DDB
 769 DDB
 770 DDB
 771 DDB
 772 DDB
 773 DDB
 774 DDB
 775 DDB
 776 DDB
 777 DDB
 778 DDB
 779 DDB
 780 DDB
 781 DDB
 782 DDB
 783 DDB
 784 DDB
 785 DDB
 786 DDB
 787 DDB
 788 DDB
 789 DDB
 790 DDB
 791 DDB
 792 DDB
 793 DDB
 794 DDB
 795 DDB
 796 DDB
 797 DDB
 798 DDB
 799 DDB
 800 DDB
 801 DDB
 802 DDB
 803 DDB
 804 DDB
 805 DDB
 806 DDB
 807 DDB
 808 DDB
 809 DDB
 810 DDB
 811 DDB
 812 DDB
 813 DDB
 814 DDB
 815 DDB
 816 DDB
 817 DDB
 818 DDB
 819 DDB
 820 DDB
 821 DDB
 822 DDB
 823 DDB
 824 DDB
 825 DDB
 826 DDB
 827 DDB
 828 DDB
 829 DDB
 830 DDB
 831 DDB
 832 DDB
 833 DDB
 834 DDB
 835 DDB
 836 DDB
 837 DDB
 838 DDB
 839 DDB
 840 DDB
 841 DDB
 842 DDB
 843 DDB
 844 DDB
 845 DDB
 846 DDB
 847 DDB
 848 DDB
 849 DDB
 850 DDB
 851 DDB
 852 DDB
 853 DDB
 854 DDB
 855 DDB
 856 DDB
 857 DDB
 858 DDB
 859 DDB
 860 DDB
 861 DDB
 862 DDB
 863 DDB
 864 DDB
 865 DDB
 866 DDB
 867 DDB
 868 DDB
 869 DDB
 870 DDB
 871 DDB
 872 DDB
 873 DDB
 874 DDB
 875 DDB
 876 DDB
 877 DDB
 878 DDB
 879 DDB
 880 DDB
 881 DDB
 882 DDB
 883 DDB
 884 DDB
 885 DDB
 886 DDB
 887 DDB
 888 DDB
 889 DDB
 890 DDB
 891 DDB
 892 DDB
 893 DDB
 894 DDB
 895 DDB
 896 DDB
 897 DDB
 898 DDB
 899 DDB
 900 DDB
 901 DDB
 902 DDB
 903 DDB
 904 DDB
 905 DDB
 906 DDB
 907 DDB
 908 DDB
 909 DDB
 910 DDB
 911 DDB
 912 DDB
 913 DDB
 914 DDB
 915 DDB
 916 DDB
 917 DDB
 918 DDB
 919 DDB
 920 DDB
 921 DDB
 922 DDB
 923 DDB
 924 DDB
 925 DDB
 926 DDB
 927 DDB
 928 DDB
 929 DDB
 930 DDB
 931 DDB
 932 DDB
 933 DDB
 934 DDB
 935 DDB
 936 DDB
 937 DDB
 938 DDB
 939 DDB
 940 DDB
 941 DDB
 942 DDB
 943 DDB
 944 DDB
 945 DDB
 946 DDB
 947 DDB
 948 DDB
 949 DDB
 950 DDB
 951 DDB
 952 DDB
 953 DDB
 954 DDB
 955 DDB
 956 DDB
 957 DDB
 958 DDB
 959 DDB
 960 DDB
 961 DDB
 962 DDB
 963 DDB
 964 DDB
 965 DDB
 966 DDB
 967 DDB
 968 DDB
 969 DDB
 970 DDB
 971 DDB
 972 DDB
 973 DDB
 974 DDB
 975 DDB
 976 DDB
 977 DDB
 978 DDB
 979 DDB
 980 DDB
 981 DDB
 982 DDB
 983 DDB
 984 DDB
 985 DDB
 986 DDB
 987 DDB
 988 DDB
 989 DDB
 990 DDB
 991 DDB
 992 DDB
 993 DDB
 994 DDB
 995 DDB
 996 DDB
 997 DDB
 998 DDB
 999 DDB
 1000 DDB
 1001 DDB
 1002 DDB
 1003 DDB
 1004 DDB
 1005 DDB
 1006 DDB
 1007 DDB
 1008 DDB
 1009 DDB
 1010 DDB
 1011 DDB
 1012 DDB
 1013 DDB
 1014 DDB
 1015 DDB
 1016 DDB
 1017 DDB
 1018 DDB
 1019 DDB
 1020 DDB
 1021 DDB
 1022 DDB
 1023 DDB
 1024 DDB
 1025 DDB
 1026 DDB
 1027 DDB
 1028 DDB
 1029 DDB
 1030 DDB
 1031 DDB
 1032 DDB
 1033 DDB
 1034 DDB
 1035 DDB
 1036 DDB
 1037 DDB
 1038 DDB
 1039 DDB
 1040 DDB
 1041 DDB
 1042 DDB
 1043 DDB
 1044 DDB
 1045 DDB
 1046 DDB
 1047 DDB
 1048 DDB
 1049 DDB
 1050 DDB
 1051 DDB
 1052 DDB
 1053 DDB
 1054 DDB
 1055 DDB
 1056 DDB
 1057 DDB
 1058 DDB
 1059 DDB
 1060 DDB
 1061 DDB
 1062 DDB
 1063 DDB
 1064 DDB
 1065 DDB
 1066 DDB
 1067 DDB
 1068 DDB
 1069 DDB
 1070 DDB
 1071 DDB
 1072 DDB
 1073 DDB
 1074 DDB
 1075 DDB
 1076 DDB
 1077 DDB
 1078 DDB
 1079 DDB
 1080 DDB
 1081 DDB
 1082 DDB
 1083 DDB
 1084 DDB
 1085 DDB
 1086 DDB
 1087 DDB
 1088 DDB
 1089 DDB
 1090 DDB
 1091 DDB
 1092 DDB
 1093 DDB
 1094 DDB
 1095 DDB
 1096 DDB
 1097 DDB
 1098 DDB
 1099 DDB
 1100 DDB
 1101 DDB
 1102 DDB
 1103 DDB
 1104 DDB
 1105 DDB
 1106 DDB
 1107 DDB
 1108 DDB
 1109 DDB
 1110 DDB
 1111 DDB
 1112 DDB
 1113 DDB
 1114 DDB
 1115 DDB
 1116 DDB
 1117 DDB
 1118 DDB
 1119 DDB
 1120 DDB
 1121 DDB
 1122 DDB
 1123 DDB
 1124 DDB
 1125 DDB
 1126 DDB
 1127 DDB
 1128 DDB
 1129 DDB
 1130 DDB
 1131 DDB
 1132 DDB
 1133 DDB
 1134 DDB
 1135 DDB
 1136 DDB
 1137 DDB
 1138 DDB
 1139 DDB
 1140 DDB
 1141 DDB
 1142 DDB
 1143 DDB
 1144 DDB
 1145 DDB
 1146 DDB
 1147 DDB
 1148 DDB
 1149 DDB
 1150 DDB
 1151 DDB
 1152 DDB
 1153 DDB
 1154 DDB
 1155 DDB
 1156 DDB
 1157 DDB
 1158 DDB
 1159 DDB
 1160 DDB
 1161 DDB
 1162 DDB
 1163 DDB
 1164 DDB
 1165 DDB
 1166 DDB
 1167 DDB
 1168 DDB
 1169 DDB
 1170 DDB
 1171 DDB
 1172 DDB
 1173 DDB
 1174 DDB
 1175 DDB
 1176 DDB
 1177 DDB
 1178 DDB
 1179 DDB
 1180 DDB
 1181 DDB
 1182 DDB
 1183 DDB
 1184 DDB
 1185 DDB
 1186 DDB
 1187 DDB
 1188 DDB
 1189 DDB
 1190 DDB
 1191 DDB
 1192 DDB
 1193 DDB
 1194 DDB
 1195 DDB
 1196 DDB
 1197 DDB
 1198 DDB
 1199 DDB
 1200 DDB
 1201 DDB
 1202 DDB
 1203 DDB
 1204 DDB
 1205 DDB
 1206 DDB
 1207 DDB
 1208 DDB
 1209 DDB
 1210 DDB
 1211 DDB
 1212 DDB
 1213 DDB
 1214 DDB
 1215 DDB
 1216 DDB
 1217 DDB
 1218 DDB
 1219 DDB
 1220 DDB
 1221 DDB
 1222 DDB
 1223 DDB
 1224 DDB
 1225 DDB
 1226 DDB
 1227 DDB
 1228 DDB
 1229 DDB
 1230 DDB
 1231 DDB
 1232 DDB
 1233 DDB
 1234 DDB
 1235 DDB
 1236 DDB
 1237 DDB
 1238 DDB
 1239 DDB
 1240 DDB
 1241 DDB
 1242 DDB
 1243 DDB
 1244 DDB
 1245 DDB
 1246 DDB
 1247 DDB
 1248 DDB
 1249 DDB
 1250 DDB
 1251 DDB
 1252 DDB
 1253 DDB
 1254 DDB
 1255 DDB
 1256 DDB
 1257 DDB
 1258 DDB
 1259 DDB
 1260 DDB
 1261 DDB
 1262 DDB
 1263 DDB
 1264 DDB
 1265 DDB
 1266 DDB
 1267 DDB
 1268 DDB
 1269 DDB
 1270 DDB
 1271 DDB
 1272 DDB
 1273 DDB
 1274 DDB
 1275 DDB
 1276 DDB
 1277 DDB
 1278 DDB
 1279 DDB
 1280 DDB
 1281 DDB
 1282 DDB
 1283 DDB
 1284 DDB
 1285 DDB
 1286 DDB
 1287 DDB
 1288 DDB
 1289 DDB
 1290 DDB
 1291 DDB
 1292 DDB
 1293 DDB
 1294 DDB
 1295 DDB
 1296 DDB
 1297 DDB
 1298 DDB
 1299 DDB
 1300 DDB
 1301 DDB
 1302 DDB
 1303 DDB
 1304 DDB
 1305 DDB
 1306 DDB
 1307 DDB
 1308 DDB
 1309 DDB
 1310 DDB
 1311 DDB
 1312 DDB
 1313 DDB
 1314 DDB
 1315 DDB
 1316 DDB
 1317 DDB
 1318 DDB
 1319 DDB
 1320 DDB
 1321 DDB
 1322 DDB
 1323 DDB
 1324 DDB
 1325 DDB
 1326 DDB
 1327 DDB
 1328 DDB
 1329 DDB
 1330 DDB
 1331 DDB
 1332 DDB
 1333 DDB
 1334 DDB
 1335 DDB
 1336 DDB
 1337 DDB
 1338 DDB
 1339 DDB
 1340 DDB
 1341 DDB
 1342 DDB
 1343 DDB
 1344 DDB
 1345 DDB
 1346 DDB
 1347 DDB
 1348 DDB
 1349 DDB
 1350 DDB
 1351 DDB
 1352 DDB
 1353 DDB
 1354 DDB
 1355 DDB
 1356 DDB
 1357 DDB
 1358 DDB
 1359 DDB
 1360 DDB
 1361 DDB
 1362 DDB
 1363 DDB
 1364 DDB
 1365 DDB
 1366 DDB
 1367 DDB
 1368 DDB
 1369 DDB
 1370 DDB
 1371 DDB
 1372 DDB
 1373 DDB
 1374 DDB
 1375 DDB
 1376 DDB
 1377 DDB
 1378 DDB
 1379 DDB
 1380 DDB
 1381 DDB
 1382 DDB
 1383 DDB
 1384 DDB
 1385 DDB
 1386 DDB
 1387 DDB
 1388 DDB
 1389 DDB
 1390 DDB
 1391 DDB
 1392 DDB
 1393 DDB
 1394 DDB
 1395 DDB
 1396 DDB
 1397 DDB
 1398 DDB
 1399 DDB
 1400 DDB
 1401 DDB
 1402 DDB
 1403 DDB
 1404 DDB
 1405 DDB
 1406 DDB
 1407 DDB
 1408 DDB
 1409 DDB
 1410 DDB
 1411 DDB
 1412 DDB
 1413 DDB
 1414 DDB
 1415 DDB
 1416 DDB
 1417 DDB
 1418 DDB
 1419 DDB
 1420 DDB
 1421 DDB
 1422 DDB
 1423 DDB
 1424 DDB
 1425 DDB
 1426 DDB
 1427 DDB
 1428 DDB
 1429 DDB
 1430 DDB
 1431 DDB
 1432 DDB
 1433 DDB
 1434 DDB
 1435 DDB
 1436 DDB
 1437 DDB
 1438 DDB
 1439 DDB
 1440 DDB
 1441 DDB
 1442 DDB
 1443 DDB
 1444 DDB
 1445 DDB
 1446 DDB
 1447 DDB
 1448 DDB
 1449 DDB
 1450 DDB
 1451 DDB
 1452 DDB
 1453 DDB
 1454 DDB
 1455 DDB
 1456 DDB
 1457 DDB
 1458 DDB
 1459 DDB
 1460 DDB
 1461 DDB
 1462 DDB
 1463 DDB
 1464 DDB
 1465 DDB
 1466 DDB
 1467 DDB
 1468 DDB
 1469 DDB
 1470 DDB
 1471 DDB
 1472 DDB
 1473 DDB
 1474 DDB
 1475 DDB
 1476 DDB
 1477 DDB
 1478 DDB
 1479 DDB
 1480 DDB
 1481 DDB
 1482 DDB
 1483 DDB
 1484 DDB
 1485 DDB
 1486 DDB
 1487 DDB
 1488 DDB
 1489 DDB
 1490 DDB
 1491 DDB
 1492 DDB
 1493 DDB
 1494 DDB
 1495 DDB
 1496 DDB
 1497 DDB
 1498 DDB
 1499 DDB
 1500 DDB
 1501 DDB
 1502 DDB
 1503 DDB
 1504 DDB
 1505 DDB
 1506 DDB
 1507 DDB
 1508 DDB
 1509 DDB
 1510 DDB
 1511 DDB
 1512 DDB
 1513 DDB
 1514 DDB
 1515 DDB
 1516 DDB
 1517 DDB
 1518 DDB
 1519 DDB
 1520 DDB
 1521 DDB
 1522 DDB
 1523 DDB
 1524 DDB
 1525 DDB
 1526 DDB
 1527 DDB
 1528 DDB
 1529 DDB
 1530 DDB
 1531 DDB
 1532 DDB
 1533 DDB
 1534 DDB
 1535 DDB
 1536 DDB
 1537 DDB
 1538 DDB
 1539 DDB
 1540 DDB
 1541 DDB
 1542 DDB
 1543 DDB
 1544 DDB
 
```

676 NSVP ----KQCENTTIVKPVSLAVPLVELTBEDKADSGMI --PP----- 802
Db 901 YCDHSOYLINTLTSITTGARRPRDPSVLIWIRKDTVAADIEOKALLEKTENLPEW 960
Qy 803 -DEEFMVLTAKASGYPGRSPRTADSGPVMGFMSTASGEVSTYNPOTLQ-SEHLDPDK 859
Db 961 TTAFTSTHLYRAAM----NQRPNVIGTISKTHGAAGNNRVRQAGNWSG-- 1006
Qy 860 IFSVNTGTAVKSMNPPIASKIEDTQNPNPIIFP-SVAERDSA---QAGRASSQS 912
Db 1007 ---LNGKNCVCPLETFIDTRTRFLIACPRGGFPI-----CPVTG--PSSGN 1045
Qy 913 AHPVTGQN---MATYGHNTNYYSSFTSKASTVLQPINPTESYGPQIPITGYSRSPSSD 966

RESULT 19
US-10-454-351-2
Sequence 2, Application US/10454351
Publication No. US20040053301A1
GENERAL INFORMATION:
APPLICANT: Quark Biotech Inc.; Paz Einat, et al.
TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF
TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF
FILE REFERENCE: 010/PCT2-US1; ENAT-75
CURRENT APPLICATION NUMBER: US/10/454,351
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: US 09/991,630
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 09/905,129
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 09/802,318
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 09/729,485
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US 09/312,216
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 2597
TYPE: PRT
ORGANISM: Rattus species
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(2597)
OTHER INFORMATION: 'x' can be any amino acid

US-10-454-351-2

Query Match 1.9%; Score 120.5; DB 12; Length 2597;
Best Local Similarity : 18.6%; Pred. No. 0.67%;
Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;

Qy 416 AGPHLAANPQTD--RDGHVILSSOSTGSNTE-----FSDYDLAICG 455
Db 274 SGALICTXPDTPLSKSILVQDNGSASTSPDFIEFGSLLNNMTXXSGNKADWCS 333
Qy 456 FGAPILLIIFYLERCDAASFTGHHGDAKYVTTGFDSPICSLICEKHTRPV--CAHT 511
Db 334 IQKE-----SRTSPTAFFENDYM-LNASFSTMVLCSDYNTIQWYQLLALYS 392
Qy 512 TVHLRQMF-----RFGQTATRQPGVFTGTMNSQSDCDPLGNAPAYLILRKGD 561
Db 383 DSPLILERKEHQLTETPSLSSRYKVALPEDFISIDEAVR-ADPPWFQEQKIVQLNRT 441
Qy 562 QTEAKATHQMDTYRATLERLFDQEQL-----LDR-----GAPCSSEG 601
Db 442 ATTLSTLQIESTDQIALPRAEMAERLWTMLMMNRKFLERTVLYGGTIALSCPGRK 501
Qy 602 -----LSSVIVDHPPFR-----RILDILRAR-EQTQENKV-----VETRD----- 639
Db 502 DPSPLHEWLADGSKYRAPPYVSEDGRILDNGKBLQWADSDGAGLTHISTDADAV 561

Query Match 1.9%; Score 120.5; DB 12; Length 2597;
Best Local Similarity : 18.6%; Pred. No. 0.67%;
Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;

Qy 416 AGPHLAANPQTD--RDGHVILSSOSTGSNTE-----FSDYDLAICG 455
Db 274 SGALICTXPDTPLSKSILVQDNGSASTSPDFIEFGSLLNNMTXXSGNKADWCS 333

456	FGAPLLARLLFYLICDAGAFTGHDALKVYTGTDFEIPCGSLCEKTRPV--	--C9HT 511
334	IQKP------SRTSPTAEEENDYM-LNASFSTNLVCSVDYNNHIQPWLQLLAYS	382
512	TYHLRQEMP-----RGCAATROPPIGVTMNSQYSDCDPLGNAYPAVLILRGKD	561
383	DSPLLERKPKQLTETPSLSRYXQVALRPEDITISEADVR-ADPFWFOQEKITVLQNLNRT	441
562	QTEAAKATMQDTYTRALFLIDEQERL-----LDR-----GAPCSSEG	601
442	ATTLSLQIOPFSTDQIALPRAENRAERLKWMILLMMNNPKLERTLVGGTTIALSPCGKG	501
602	----LSSIVVDHPTFR-----RILDTLRARI-QTTTQPMKV-----VTFRD-----	639
502	DPSPHLWELADGSKVRAPYVSEDPGRGKIDNGKELOMNADSPDAGLYCHCISNDADADV	561
640	--YKTR--EGLSEATHSMALTFDPSGAF---CPTINFLVKRTHLAVYQDLALSQCHCV	691
562	LTYRITYVEPYGESTHDGSVQHTVTYTGELDLPCLSTG-----VPDASTS-WI	608
692	FYQQQVEGRNRFRNQFQPVLRRRFVLDLNGCFISTRISTRVTLSECPVS-APNP-----	743
609	LPGNTVFSQPSRDR-----QILNNTGTRILQVT PKDQGHYQCYAANPSGADFSS	657
744	-----LGQDAPAGRTPEFGDLARVSVEYTDRLYKRNRYVFSGCNTNUSEAAAR	791
658	FKVSVQKGQRMVEHDRAGGSIE-PRSSVSVLRQPSLK---LSSALTSGEAGK-	711
792	LVGLASAYQREKVRDMLHGALG-FLIKOPHGLLFPRGMPPNSKSPNPOWFVTLQ--R	847
712	-----VSGYTHRKNGKHERDLTHRRRGTSITLRFRE-HRQLPLSARRIDPQRWAILEKARK	765
848	NQMPADK-THEETTT-----IAAVKRKTEYYAAINFNFNLPPCTIGELAQFTMANLILK	900
766	NSVP-----KKQENTTVKPVPLAYFLVLTDEEKDSGM-----PP-----	802
901	YCDHSQYUJNTLISITGARRPRPSVSHWIRKDVTSASDIEQKAKALLEKTYENLPFW	960
803	--DEFEWVLUKTRASGVGRSPPTADSQPNHGFMTSISASGETEVSTVNQPTLQ-SEHLPDFK	859
961	TIAFTSTHLVRAAM-----NORPMVVULGISISKYGAAANNRVFOAGNWSG-----	1096
860	LFSYVNTGATVTKSNPSTIASKIEDTNQNPILLPP-SVAEIRDSA-----QAGRASSQS	912
1007	--INGGKNCVCPPLTFDPRRPFIACPRGFFI-----CPVTG--PSGN 1045	
913	AHPYTTGGN---MATYGHNTYSSSETSKASTVLQFINTPTESYGPQIPITGVSRSSSD	966

LENGTH: 2597
 TYPE: PRT
 ORGANISM: Rattus e
 FEATURE:
 NAME/KEY : miss-fee
 LOCATION: (1)...(2597)
 OTHER INFORMATION
 JS-10-454-351-13

Query Match	
Best Local Similarity	Consecutive Matches
416 AGPHLAAM : 274 SGAFLCTH	416 AGPHLAAM : 274 SGAFLCTH
456 FGAPILAF : 334 IQKE-----	456 FGAPILAF : 334 IQKE-----
512 TVERHLRQW : 383 DSPLILE	512 TVERHLRQW : 383 DSPLILE
562 QTEAAKAK : 442 ATTLSTLLE	562 QTEAAKAK : 442 ATTLSTLLE
602 -----ISS : 502 DPSPHLEY	602 -----ISS : 502 DPSPHLEY
640 --YKIR-- : 562 LTYRITVY	640 --YKIR-- : 562 LTYRITVY
692 FYGQQVEE : 609 LPGNTVFPE	692 FYGQQVEE : 609 LPGNTVFPE
744 ----- : 658 FKVSVKQI	744 ----- : 658 FKVSVKQI
792 LVGLASA : 712 ---VSG	792 LVGLASA : 712 ---VSG
848 NQMPADKII : 766 NSVP---	848 NQMPADKII : 766 NSVP---
901 YCDHSQYV : 803 -DEFM	901 YCDHSQYV : 803 -DEFM
961 TTAFFSTI : 860 LFSVTING	961 TTAFFSTI : 860 LFSVTING
QY 1007 ---INGGI : Dbb 913 AHPVTGG	QY 1007 ---INGGI : Dbb 913 AHPVTGG

RESULT 22
 US-09-729-485A-2
 Sequence 2, Applica
 Publication No. US2
 GENERAL INFORMATION
 ; APPLICANT: Quark B
 ; ATTORNEY: Einat
 ; INVENTOR: Einat

766 NVPV --- KQGNTTTRPVPLAVPVLTBEKUSGMN -- PP----- 806
 901 YCDHSQYLINTLTSITGARRPRDPSSVLMWIKDVTSAADIEQAKALLEKTENILPELN 960
 803 --DEEFNVYLKTKASGTEGRSPTAADSGPVNQGFMSTIASGIEVSTNPOTIQ-SEHPDFK 859
 961 TIAFTTFLVRAM ----- NORPAPVLGISISKHGAACNRYFOAGNTSG-- 1000
 860 LFSVNTGTAVTKSMSPIASKIEDTTNQNPIIIFP-SVAELRDSA----QAGRASSOS 912
 1007 --LNGGERKNCVPLFTFTRTRFLIACPRGGTI---CPVTG--PSSGN 1045
 913 AHPTVGEN --- MATIGHTNTYSSPSKASATVQLBPNPTESYGPQIPITGVSPSSSD 966

3
 39-485A-10
 39-485A-10 Application US/09729485A
 39-485A-10 Application No. US2002020202A1
 39-485A-10 ALL INFORMATION: AND USES THEREOF
 39-485A-10 CANT: Quark Biotech, Inc.
 39-485A-10 CANT: Einat, Paz
 39-485A-10 CANT: segev, Orbit
 39-485A-10 CANT: Skaliter, Rami
 39-485A-10 CANT: Einstein, Elena
 39-485A-10 CANT: Faerman, Alexander
 39-485A-10 CANT: INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PROD
 39-485A-10 CANT: OF INVENTION: AND USES THEREOF
 39-485A-10 REFERENCE: S40579-2007
 39-485A-10 CURRENT FILING DATE: 2000-12-04
 39-485A-10 APPLICATION NUMBER: 09/729,485
 39-485A-10 FILING DATE: 2000-12-04
 39-485A-10 APPLICATION NUMBER: 09/632,862
 39-485A-10 FILING DATE: 2000-08-04
 39-485A-10 APPLICATION NUMBER: 60/207,821
 39-485A-10 FILING DATE: 2000-05-30
 39-485A-10 APPLICATION NUMBER: 60/084,944
 39-485A-10 FILING DATE: 1998-05-11
 39-485A-10 APPLICATION NUMBER: 60/085,673
 39-485A-10 FILING DATE: 1998-05-15
 39-485A-10 SEQ ID NOS: 22
 39-485A-10 AWARE: PatentIn version 3.1
 39-485A-10 NO: 10
 39-485A-10 3TH: 2597
 39-485A-10 3: PRT: Organism: Rattus species
 39-485A-10 4: TURE:
 39-485A-10 5: KEY: MISGFEATURE
 39-485A-10 6: FEATURE: (1). (255)
 39-485A-10 7: INFORMATION: "xaa" can be any amino acid
 39-485A-10
 Match 1.9%; Score 120.5; DB 12; Length 2597;
 Local Similarity 18.6%; Prod. No. 0 67; Mismatchs 287; Indeels 233; Gaps 40
 es 145; Conservative 113; Mismatchs 287; Indeels 233; Gaps 40
 416 AGPHIAANPQTD---RDGHVLSSTGSTGSNTT-----FSYDVLALJCG 455
 274 SGAFCLCTKETIDPRLSKSLVTPQDNGASASTSQQDFLEPPFGSLSLNMTXXSGNKADMVC 333
 456 FGAPILLARLFLYERCDAGAFTGCHGDAKYVTTGDFSEIIPCSCUCEKHTRPV---CAHT 511
 334 IQKPL-----SRTSPTAFTEEENDYIM-LNAsFSTNLVCEVDYHIIQPYWQLLALYS 382
 512 TVHRILQRMP-----RFGGATROPICGIVGTMQSYSDOPDPLNYAYPLILRKPGD 561
 383 DSPILLERQPLTETPSLSRYKQYALFEPDITISIEDVR-ADPFWFOQEKLWVQLNRT 441
 562 QTEAAKATMVDTYATLBLSFLIDEQERL-----LDR-----GAPCSBEG 601
 442 ATTLSLTLQIOFSTDQIALPRAEMRAEILKWTMMLMMNNPKLERTVLNGGTIALSCPKG 501

RESULT 24
US-09-729-485A-13
Sequence 13, Application US/09729485A
GENERAL INFORMATION:
Publication No. US2002002206A1
APPLICANT: Quark Biotech, Inc.
Binat, Paz
Segev, Orbit
Skaliter, Rami
APPLICANT: Feinstein, Elana
APPLICANT: Faerman, Alexander
TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF
FILE REFERENCE: 540579-2-207
CURRENT FILING DATE: 2000-12-04
PRIORITY APPLICATION NUMBER: US/05/729,485A
PRIORITY FILING DATE: 1998-05-11
PRIORITY APPLICATION NUMBER: 09/729,485
PRIORITY FILING DATE: 2000-12-04
PRIORITY APPLICATION NUMBER: 09/632,862
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/107,821
PRIORITY FILING DATE: 2000-05-10
PRIORITY APPLICATION NUMBER: 60/084,944
PRIORITY FILING DATE: 1998-05-11
PRIORITY APPLICATION NUMBER: 60/085,673
PRIORITY FILING DATE: 1998-05-04
PRIORITY APPLICATION NUMBER: 60/107,821
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 2597
TYPE: PRT
ORGANISM: Rattus species
FEATURE: MISC FEATURE
NAME/KEY: (1)-(2597)
OTHER INFORMATION: "Xaa" can be any amino acid

US-09-729-485A-13
Query Match 1.9%; Score 120.5; DB 12; Length 2597;
Best Local Similarity 18.8%; Pred. No. 0.67;
Matches 145; Conservative 113; Mismatches 287; Index 233; Gaps 40;
Qy 416 AGPHLAMPQD--RIGHVLLSQSTGSSNT--FSYDYLALIGC 455
Db 274 SGAFLCKPTIDPSLISKSLSVQEDNGSASTSPQDIEPFGLSSLNMTXXSGNKADMVC 333
Qy 456 FGAFLARLLFTYLERCAGAFIGGHGDALKVGTGTDSEIPCSLCRHTREV---CAHT 511
Db 334 IQXP-----SRTSPTAEEENDYM-LNASSSTNLVCSVDYNHIQPWQLLALYS 382
Db 512 TYVERLQROMP-----RGQATROPICVGFGTMNSOYSDCDPLQNYAAYPLILRKPGD 561
Db 333 DSPLILRKPOJETPLSSRTRKVAIRPEDIITSIAEADYD-ADPFWFQQEKTVLQJNRT 441
Qy 562 QTEAAKATMMDTYRATERLFIDLEQERL-----LDR-----GAPCSSEG 601
Db 442 ATTLSITQFSTDQAQALPRAEMRARRKWTMILMNPNPKLERTLVGGTIALSGPGK 501
Db 602 -----LSQVIVDEPTFR-----RILDITDARIE QTTOQMKTZ-----VETRD---- 639
Db 502 DPSPLHFLWILADGSKVTAPEYSEDGRLLIDKNGKLEQMAFSDAGLYHC1STNDADADV 561
Qy 640 --YKIR-EGLSBEATHSMALTFDPSGAF---CPTINFLVYERTHLAVVODIALSQQHCV 691
Db 562 LTRITRVEPYKPSHTDSGVQHTVTTBTLLPCLSG-----VPDASIS--WI 608
Db 692 FYGQQVEGRNFRNQFOFPVLRRFVDFNGCFISTRSTVTLSEGPSV--APNPT---- 743
Db 609 LPGNNTVFSQPSRDR-----QIANNGTRILQQT-PADQGHYCQVAANPSGADFSS 657
Qy 744 -----LGQDAPAGRTEGDGLALARSYEVIRDIRVKRNVRVFFGNCNTNLSEARAR 791
Db 658 FKVSVQKGQRMYEHDRDAGGSGLGE PNSSYSLKOASLK---LQSALTGSEAGKQ- 711
Qy 792 LVGLASAYQRQEVRVDMHLHAGL-FLIKQFHGLFPRGMPPNKSPPNPQWFNTLQ---R 847
Db 712 ---VSGERKNGERDLHRRRGSDFSTRRFRF-HRQLPLSARRIDQFRWALLEXAKK 765
Qy 848 NQMPADKUJTHEETT-----TAAVKRFTEEYAAlPINLPPTCIGELAQFYMANLILK 900
Db 766 NSVP--KKQENTTYKPVPLAYLVELTDEKDASGM--FP----- 802
Qy 901 YCDHSQYLINTLTSITGARRPRDSSVLMKIRDTSADIEQTKALLEKTEENLPILW 960
Db 860 LFSVTINGTAVTKMSNPIASKIEDTNQNTIIFF-SVAATRDSA-----QAGRASSQS 912
Qy 1007 --LNGGKVNCPFLFTDRTRRFIIACPRGGFI-----CPVNTG--PSSGN 1045
Db 913 AHPVIGON--MATYGHNTYSSFTSKASTVLIQDINPTESYGPQIPITQVSRFSSSD 966
Qy 744 -----LGQDAPAGRTEGDGLALARSYEVIRDIRVKRNVRVFFGNCNTNLSEARAR 791
Db 658 FKVSVQKGQRMYEHDRDAGGSGLGE PNSSYSLKOASLK---LQSALTGSEAGKQ- 711
Qy 792 LVGLASAYQRQEVRVDMHLHAGL-FLIKQFHGLFPRGMPPNKSPPNPQWFNTLQ---R 847
Db 712 ---VSGERKNGERDLHRRRGSDFSTRRFRF-HRQLPLSARRIDQFRWALLEXAKK 765
Qy 848 NQMPADKUJTHEETT-----TAAVKRFTEEYAAlPINLPPTCIGELAQFYMANLILK 900
Db 766 NSVP--KKQENTTYKPVPLAYLVELTDEKDASGM--FP----- 802
Qy 901 YCDHSQYLINTLTSITGARRPRDSSVLMKIRDTSADIEQTKALLEKTEENLPILW 960
Db 860 LFSVTINGTAVTKMSNPIASKIEDTNQNTIIFF-SVAATRDSA-----QAGRASSQS 912
Qy 1007 --LNGGKVNCPFLFTDRTRRFIIACPRGGFI-----CPVNTG--PSSGN 1045
Db 913 AHPVIGON--MATYGHNTYSSFTSKASTVLIQDINPTESYGPQIPITQVSRFSSSD 966
Qy 961 TTATSTHLVRAAM-----NOREMYLGISSISKTHGAAGNNRVFOAGNWGG- 1006
Db 860 LFSTVNGTAVTKMSNPIASKIEDTNQNTIIFF-SVAATRDSA-----QAGRASSQS 912
Qy 1007 --LNGGKVNCPFLFTDRTRRFIIACPRGGFI-----CPVNTG--PSSGN 1045
Db 913 AHPVIGON--MATYGHNTYSSFTSKASTVLIQDINPTESYGPQIPITQVSRFSSSD 966
RESULT 25
US-09-802-318-2
Sequence 2, Application US/09802318
GENERAL INFORMATION:
Publication No. US20020086825A1
APPLICANT: Eint, et al.
TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF
FILE REFERENCE: 540579-2-207
CURRENT FILING DATE: 2000-12-04
PRIORITY APPLICATION NUMBER: US/05/729,485A
PRIORITY FILING DATE: 1998-05-11
PRIORITY APPLICATION NUMBER: 09/729,485
PRIORITY FILING DATE: 2000-12-04
PRIORITY APPLICATION NUMBER: 09/632,862
PRIORITY FILING DATE: 1998-05-15
NUMBER OF SEQ ID Nos: 22
SEQ ID NO 13
LENGTH: 2597
TYPE: PRT
ORGANISM: Rattus species
FEATURE: MISC FEATURE
NAME/KEY: (1)-(2597)
OTHER INFORMATION: "Xaa" can be any amino acid

PRIOR FILING DATE: 2000-05-30
 SOFTWARE: Seq ID Nos: 25
 SEQ ID NO: 2597
 TYPE: PRT
 ORGANISM: rattus species
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) -(2597)
 OTHER INFORMATION: 'x' can be any amino acid
 US-09-802-318-2

Query Match 1.9%; Score 120.5; DB 12; Length 2597;
 Best Local Similarity 18.6%; Prd. No. 0.67; Mismatches 287; Gaps 40;
 Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;

Length: 2597
 SEQ ID NO: 10
 TYPE: PRT
 ORGANISM: Rattus sp.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) -(2597)
 OTHER INFORMATION: 'x' can be any amino acid
 US-09-802-318-10

Query Match 1.9%; Score 120.5; DB 12; Length 2597;
 Best Local Similarity 18.6%; Prd. No. 0.67; Mismatches 287; Gaps 40;
 Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;

416 AGPHLAANPQTD--RDPHVLSSQSTGSANTE-----FSYDYLALICG 455
 512 TVHLRLRQMP-----RFGQATROPIGVFGTMNSQSPCDPLGNYAPYLILRKPGD 561
 383 DSPLLERKQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWQKEKIVLQNLRT 441
 562 CTEAAKATMQDTYRATLERLFILEQSR-----LDR-----GAPSSSEG 601
 442 ATTLSLTLQQFSTDQAIAIPRAEMRABRILKWTMILMMNNPKLERTLVGGITALSPKG 501
 602 ----LSSVYIVDHPTR----RILDILRARIE-QTTQFMKVY----VETRD----639
 502 DPSPHLENTLADGSKVRAFPYVSEDGRILLDKNCKLELQMAADSFDAGLYHC1STNDADAV 561
 640 --YKIR--EGLSEATHSMALTFDPSGAF---CPTINFLVKRTHLAVQVDIALSQCVC 691
 562 LTYRITVVPPYGETSDHSGVQHTVVTGETLDIPLCLSTG-----VPDASIS--WI 608
 692 FYGCGVEQRGNFRNFOPVLRREPVDFGQF1G1F1STR1TLLSEGPVS--APNPT----743
 609 LPGNTVFSQPSDR-----QILNGTURILQVTP-PRODGHYOCVAANPSGADFSS 657
 744 -----LGQDAPAGRTPDGLALARSYEVIRDTRVNRRVVFSGNCTNLSEARAR 791
 658 FKVSQVKXKQRMVHDREGGSGGE--INSSVSKOPASLK---USASALTGEAQKQ- 711
 792 LVGLASAYQROKEQKVDMLHGALG-FLKQFHGLEPRGMPPNSKSNPQWFVLLQ--R 847
 712 ---VSGVHRKXKHDLIIRRGDSTLRFRE-HRROQPLSARRIDQVRAALLKAK 765
 848 NQMPADKLTHEEIT----IAVFRTEYAAINTNINLPPTCDELAQFYMANLILK 900
 766 NSVP----EKQENTTIVKPYPLAFLVLTDEERDASGM1--PP-----802
 901 YCDHSQYLNLTSLITGARRPRDESSVHWRDVTSAADFTQAKALLEKTENPEW 960
 803 --DEFMVTKTAKGVGRSPADSGPYNHGFNTSIASGTEVSTVNQTLQ_SEHNPDFK 859
 961 TTAFTSTHLYRAAM-----NORMVYLGISISKYGAAGNNRVFOAGNWSG--1006
 860 LFSVTINGTAVTKSNPSTASKIEDTTNQNPPII:FP-SVAEIRDSDA----DAGRASSQS 912
 1007 ---LNGKXNCPLTFDRTPRFLACPRGF1-----CPVTTG----PSSGN 1045
 913 AHPYTGNN---MATYGHNTYSSFTSKASTVLIQPINPTESYQPQIPYGSRPSSD 966
 RESULT 25
 US-09-802-318-10
 ; Sequence 10, Application US/09802318

Publication No. US20020086825A1
 GENERAL INFORMATION:
 APPLICANT: Binat, et al
 TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS EXPRESSION PRODUCTS THEREOF
 LENGTH: 2597
 FILE REFERENCE: 540579-2007.1
 CURRENT APPLICATION NUMBER: US/09/802,318
 PRIORITY APPLICATION NUMBER: 97/632,862
 PRIOR FILING DATE: 2001-03-08
 PRIORITY FILING DATE: 2000-08-04
 PRIORITY FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 10
 TYPE: PRT
 ORGANISM: Rattus sp.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) -(2597)
 OTHER INFORMATION: 'x' can be any amino acid
 US-09-802-318-10

Query Match 1.9%; Score 120.5; DB 12; Length 2597;
 Best Local Similarity 18.6%; Prd. No. 0.67; Mismatches 287; Gaps 40;
 Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;

416 AGPHLAANPQTD--RDPHVLSSQSTGSANTE-----FSYDYLALICG 455
 274 SGAFLCTKPTIDPSLKSLSKSVTOQDNGSAASTSFPQDFIEPFGSLSLNMTXSGNKADMVCS 333
 Qy 456 FGAPLARLFLYLERCDAGAFTGGHGDALKYKVTGDFOSEIPOSLEBHRTRPV---CAHT 511
 Db 334 IQKP-----SRTSPTAEIFENDYM--INASFSTNLVCSVDYNNHIQPYWOLLALYS 382
 Qy 512 TVHLRLRQMP-----RFGQATROPIGVFGTMNSQSPCDPLGNYAPYLILRKPGD 561
 Db 383 DSPLLERKQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWQKEKIVLQNLRT 441
 Qy 562 CTEAAKATMQDTYRATLERLFILEQSR-----LDR-----GAPSSSEG 601
 Db 442 ATTLSLTLQQFSTDQAIAIPRAEMRABRILKWTMILMMNNPKLERTLVGGITALSPKG 501
 Qy 602 ----LSSVYIVDHPTR----RILDILRARIE-QTTQFMKVY----VETRD----639
 Db 334 IQKP-----SRTSPTAEIFENDYM--INASFSTNLVCSVDYNNHIQPYWOLLALYS 382
 Qy 512 TVHLRLRQMP-----RFGQATROPIGVFGTMNSQSPCDPLGNYAPYLILRKPGD 561
 Db 383 DSPLLERKQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWQKEKIVLQNLRT 441
 Qy 456 FGAPLARLFLYLERCDAGAFTGGHGDALKYKVTGDFOSEIPOSLEBHRTRPV---CAHT 511
 Db 334 IQKP-----SRTSPTAEIFENDYM--INASFSTNLVCSVDYNNHIQPYWOLLALYS 382
 Qy 512 TVHLRLRQMP-----RFGQATROPIGVFGTMNSQSPCDPLGNYAPYLILRKPGD 561
 Db 383 DSPLLERKQLTETPSLSSRYKQVALRPEDIFTSIEADVR-ADPFWQKEKIVLQNLRT 441
 Qy 562 CTEAAKATMQDTYRATLERLFILEQERU-----LDR-----GAPSSSEG 601
 Db 442 ATTLSLTLQFSTDQAIAIPRAEMRABRILKWTMILMMNNPKLERTLVGGITALSPKG 501
 Qy 602 ----LSSVYIVDHPTR----RILDILRARIE-QTTQFMKVY----VETRD----639
 Db 502 DPSPHLENTLADGSKVRAFPYVSEDGRILLDKNCKLELQMAADSFDAGLYHC1STNDADAV 561
 Qy 640 --YKIR--EGLSEATHSMALTFDPSGAF---CPTINFLVKRTHLAVQVDIALSQCVC 691
 Db 562 LTYRITVVPPYGETSDHSGVQHTVVTGETLDIPLCLSTG-----VPDASIS--WI 608
 Qy 692 FYGCGVEQRGNFRNFOPVLRREPVDFGQF1G1F1STR1TLLSEGPVS--APNPT----743
 Db 609 LPGNTVFSQPSDR-----QILNGTURILQVTP-PRODGHYOCVAANPSGADFSS 657
 Qy 744 -----LGQDAPAGRTPDGLALARSYEVIRDTRVNRRVVFSGNCTNLSEARAR 791
 Db 658 FKVSQVKXKQRMVHDREGGSGGE--INSSVSKOPASLK---USASALTGEAQKQ- 711
 Qy 792 LVGLASAYQROKEQKVDMLHGALG-FLKQFHGLEPRGMPPNSKSNPQWFVLLQ--R 847
 Db 712 ---VSGVHRKXKHDLIIRRGDSTLRFRE-HRROQPLSARRIDQVRAALLKAK 765
 Qy 848 NQMPADKLTHEEIT----IAVFRTEYAAINTNINLPPTCDELAQFYMANLILK 900
 Db 766 NSVP----EKQENTTIVKPYPLAFLVLTDEERDASGM1--PP-----802
 Qy 901 YCDHSQYLNLTSLITGARRPRDESSVHWRDVTSAADFTQAKALLEKTENPEW 960
 Db 803 --DEFMVTKTAKGVGRSPADSGPYNHGFNTSIASGTEVSTVNQTLQ_SEHNPDFK 859
 Qy 961 TTAFTSTHLYRAAM-----NORMVYLGISISKYGAAGNNRVFOAGNWSG--1006
 Db 860 LFSVTINGTAVTKSNPSTASKIEDTTNQNPPII:FP-SVAEIRDSDA----DAGRASSQS 912
 Qy 1007 ---LNGKXNCPLTFDRTPRFLACPRGF1-----CPVTTG----PSSGN 1045
 Db 913 AHPYTGNN---MATYGHNTYSSFTSKASTVLIQPINPTESYQPQIPYGSRPSSD 966
 Db 803 --DEFMVTKTAKGVGRSPADSGPYNHGFNTSIASGTEVSTVNQTLQ_SEHNPDFK 859
 Qy 961 TTAFTSTHLYRAAM-----NORMVYLGISISKYGAAGNNRVFOAGNWSG--1006

RESULT 27
 US-09-802-318-13
 / Sequence 13, Application US/09802318
 / GENERAL INFORMATION:
 / APPLICANT: Binat, et al
 / TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF
 / FILE REFERENCE: 540519-2007.1
 / CURRENT FILING DATE: 2001-03-08
 / PRIOR APPLICATION NUMBER: 09/622,862
 / PRIOR FILING DATE: 2000-08-04
 / PRIOR APPLICATION NUMBER: 60/207,821
 / PRIOR FILING DATE: 2000-05-30
 / NUMBER OF SEQ ID NOS: 25
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO: 13
 / LENGTH: 2,947
 / TYPE: PT
 / ORGANISM: Rattus sp.
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (1) -(259)
 / OTHER INFORMATION: 'x' can be any amino acid
 US-09-802-318-13

Query Match 1.9%; Score 120.5; DB 12; Length 259;
 Best Local Similarity 18.6%; Pred. No. 0.67; Mismatches 113; Indels 233; Gaps 40;
 Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;

Query 416 AGPHIAANPDTD--RDGHFLSSQSTGSSNTB-----FSDYALIJC 455
 Db 274 SGAGIATCTKPIDPSIKSKRCDAGFTGGDAKXVGTFSDFSEIIPCGSLSNMTXXSGNKADYVC 333
 Query 456 FGAPLLARLFLYLERCDAGFTGGDAKXVGTFSDFSEIIPCGSLSNMTXXSGNKADYVC 333
 Db 334 IOKP-----SRTSP1PAFTENDYM--LNRFSPTNLVCSDYNEHQPTWQLLLYS 382
 Query 512 TVHRLQRQMP-----RGFQATRQPIGVFETMNSQYSDCPLGNHYAPYLIRKEGD 561
 Db 383 DSPLIERKEPOLTETPSLSSRYKQALRPEDIFTSIEADR-ADPFMEQQEKIVLQNR 441
 Query 562 QTEAKAKATQDVTYRATLERLFDIQLQERL-----LDR-----GAPCSSEG 601
 Db 442 ATTSTLQDFSTDQIAJALPRAENRAERLKVWTMILMNPNPQCLERTVLYGGTIALSCPGK 501
 Query 602 -----LSSVIVDHPFR-----RILDILRARIE-QTTQPMKV-----VETRD---- 639
 Db 502 DPSPLIEWLADGSKVRAPIVSEDRILLDKNGKLELQMDASTDAGLYHCISNDADAV 561
 Query 640 --YKIR--EGLSEATHSMALTFDPYSGAF---CPITNFLVRETHLAYQDIALSOCHCV 691
 Db 562 LTYRTTVVEYGESTDHSGVQHTVVTGETLDPFLSTG-----VPDASIS---WI 608
 Query 692 FYGQOVEGRNFRNQFQPVLRRRFYDLENGGFISTRSITYTLSGPVS--AAPT---- 743
 Db 609 LPGNTVFSQSPRDR-----QILNNGTTLRLQVTF-KDQSHYQCVANPNSGADFSS 657
 Query 744 -----LGODAPAGRTFGDGLARVSVEVTDVIRKRNVRVFSGNCTNLSEARAR 791
 Db 658 FKVSVKQKGORMVHEDREAGSGLGE-PNISVSLKOPASK---LSASALTGSEAGRK- 711
 Query 792 LVGLASAYQFQEKRVDMLHAGL-FLIKOFHGLLPQRGMPNSPKSPNIPQWFTWLLQ--R 847

Db 712 ----VSGVHRKNKHDLIHRRGDSTLRRPRE--HRRQLPLSARRIDPQRWAALLEKARK 765
 Query 848 NOMPADKLTHEITT-----IAAVKRFEPEYYAAINFINLPTCTGELAQFYMANLILK 900
 Db 766 NSVP---KRCENTTYKPVPLAVPLVLTDEKDAGSMI--PP----- 802
 Query 901 YCDHSQQLINTLTSITGARRPRDPSVLEMKRDVUTSAIDIETQAKALLEKTENLPELN 960
 Db 803 --DEEFMVLKTKASGVGRSPTAQSSPVNNGEMTSASGTEVSTNPQTLO-SEHLPDFK 859
 Query 961 TIAFTSPHLVRAAM-----NQRPMVVLGIISIKYHGAAGNVRQAGHWSG- 1006
 Db 860 LFSVTINGTAVTKMSNPSIASKIEDTINQNPIIIFP-SVAETRDSA----QAGRASSQS 912
 Query 1007 ---LNGCKNVCPBLFTPDRTRFLIACRGFFI-----CPVIG--PSSGN 1045
 Db 913 AHPPVGGN---MATYGHINTYSSFTSKASTVLPQINPTESYGPQIPTGYSRPSSSD 966

RESULT 28
 US-10-329-079-11
 / Sequence 11, Application US/10329079
 / Publication No. US0030198981A1
 / GENERAL INFORMATION:
 / APPLICANT: FARNET, Chris
 / APPLICANT: ZAZOPOULOS, Emmanuel
 / APPLICANT: STAFFA, Alfredo
 / TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
 / FILE REFERENCE: 3.002-11US
 / CURRENT APPLICATION NUMBER: US/10/329,079
 / CURRENT FILING DATE: 2002-12-24
 / NUMBER OF SEQ ID NOS: 66
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO: 11
 / LENGTH: 5245
 / TYPE: PT
 / ORGANISM: Streptomyces fradiae
 US-10-329-079-11

Query Match 1.9%; Score 120; DB 14; Length 5245;
 Best Local Similarity 20.2%; Pred. No. 2.6; Mismatches 434; Indels 464; Gaps 68;
 Matches 262; Conservative 113; Mismatches 434; Indels 464; Gaps 68;
 Query 102 PSSAAPVULTRACNAARERFGFSRCQGP-----VDGAVETTGAEICTRL-----GL 147
 Db 464 PAAAEPAADEGLAEVCDTFARQQAATPEAPAVVGCPVALFAEADAVSRLARLLISRGA 523
 Query 148 EPENTILLYVTTALFKEAVENTFLHYGGGLDIVHNGDVTRIPFLPYQLFMPDVNRLV 207
 Db 524 GP-----VRYVACLDENRALWTTV-----LAVLRSGAHVPL----- 556
 Query 208 PDPENTHRSIGEGFPVTPPYNTGLCHLHDCCVIAPIAVALRVENVTAVARGAAHIAF- 266
 Db 557 -DPRSPER-----LAVERD-----VAPPLVLAERATEAAVADLAAPFLV 597
 Query 267 DENHEAV-----LPPDITTYTYFQSSSSG-----TTTARG----A 297
 Db 598 DDPSTERAIDALDGPVTDADRTAPLPGHAAVYVHTSGSTGRPKGVTVDHRLGSRLQ 657
 Query 298 RRNDVNSTSKEPSPSG-GFERLASTI-----MAADTAHLA----- 330
 Db 658 HRRVTSRIRISAGGPQRAAHVSSSFSDASWDPLLMVAGHELMIDDLRFDPPGVAY 717
 Query 331 -----EVIFTGTYEE-----TPT----DIKEWMFNGMEGLPRLNAL 365
 Db 718 FDRRIDYVDLDTPTYPRSLLDGLLEEGFPCPSLVVALGGEMDGEIWERLRAAARTAM 777
 Query 366 GSY----TARYA-----GVIGAMVFSPSNALSYLTVEEDSGNTNEAKDGGGPFSN 411
 Db 778 NTYGPTRTAVAVVTLGDLDPGTGRPV--PRWAY--VLDAGLRPVPGVIGELI-- 830
 Query 412 PYQFAGBHLAANPOTDRDGHVLSQSTGSSNTFSDYDYLALICGFCA-----LLAR 463

831 ---LAGPGVARGYLQO---HALTAER-----FVACPFKPKGERMYRTGDLAR 871
 465 L----LFLYLERCD-----AGAF----TGCNGDALKYV 487
 Qy 872 WLPDPGHLYVGRGDEQVKIRGPRIEGVEAAIRELEGVAAAAVTRDGTTRLGYV 931
 Db 488 TGTFSEFCISCEKHTRPVCHTTVHLRQMP----REFQATRQPISGFETMSQX 541
 Qy 932 VGPFPAD-----DARUPA---EVLAIRDRPDLHIVPSAFLRLPNTSGKLDR 981
 Qy 542 SDCDPLGNYAPILLRKKGQDTAAKATMQDTRYRATERFLDQEERLLRGAPSSCG 601
 Db 932 --ALPAZPDADEPDAGRPP-----RTAELRECVCAFLAEVL-----G 1014
 Qy 602 LSSVIVDHTHTFLDTRARIEQTTOMKVLIVEVDYKIREGLSPTHATSMALTPDYS 661
 Db 1015 AGSYGIDDDFFGRGDSIIS-----IQLVGSAR--PAGL---TFTVTRQFELR 1058
 Qy 662 GAFCPITNFVKESTHALVVQDIALSQCCVFYQQVEGRNFRNQFQEVLRFDLFGGG 721
 Db 1059 PAALAA---ARRTDAAGDEDPLA-----VGP-----LPLPVVAAETLAAAGG 1098
 Qy 722 FISRSITVILSEGPSPVSAAPNPTLGODAPAGRTEGDGLARVSVEV-----IRDIVYKNR- 774
 Db 1099 PVISYNQSVVLAASQVSPDAAFPDV--RDALQALUDRHDALRHAPAAGPGRWDLRYBEAG 1156
 Qy 775 VVFSGNC-----TNLS---EAARALVCLASAYQRQEKRVDMLHAGLGFLLKQFHGLLF 826
 Db 1157 TVAEERCLRIDATGMSDELLAQAQAAAPTA---BACLDPLAGL-----VSAAWFD 1206
 Qy 827 RGMPP-----NSKSPNPKW-----FWTLORNQMPADKLTBEITTIAAVRF 869
 Db 1207 RGDPRGRLVTVHLAVDGVSVRILLGDLREKWRBARRRDELPTGTSLRTWT--RL 1264
 Qy 870 TEYAAATINFNLNPCTCIGBLAQFYMANLILCYCDHSOYLINTLTSITGTAIRPRD-PSS- 927
 Db 1265 TERAT-----DPAVTAQL-DHWTATLADGPAPGSPRLDRTRDVTATSIVSGELPASL 1316
 Qy 928 -----VLIHWI-RKDVTSAADIETOKAALLEKTENL---956
 Db 1317 TTDILGPAAFAFAGVNLLTATPALAIAHVGEEADAPVLDLESHG----RTERLVPG 1371
 Qy 957 PELWTTA-FTSPHLVRAAMNQRPMVYUUGISISKHYGAAGN----NRVFOAGNWGLNG 1009
 Db 1372 ADLSRTVGFNTSVEPVRLAAGR---VTAADIAERAAPAVGDAIKRKEQLRAPVDPDGLGH 1427
 Qy 1010 G--KNVCP-----LFPFDYRTRFIIACPRGEGICPV--TGPSSGNRETTLSDO 1053
 Db 1428 GLRLRHNPTAPLPRLGLRARFESFNLYGRFAAEQGASEDSWNLGSQPGQHPDPTLDHE 1487
 Qy 1054 VRGILIVS----GAMYVOLAIATVVAZGARAQHMAFDWLSLTDDDEFLARDLZBLHDQ 1108
 Db 1488 IEVNVTAEGPDPRLTRWYTAGL-----L7EEB-----1518
 Qy 1109 IIOTLETPTVGEALEAVKILDEKTTAG-DGETPTNIA 1145
 Db 1519 -VRRLTRSLSL-ALHAY-VGHATAEGAGGLSPSDVA 1551

RESULT 29
 US-10-425-114-71520
 Sequence 71520, Application US/10425114
 Publication No. US20040034888A1
 GENERAL INFORMATION:
 APPLICANT Liu, Jingdong
 APPLICANT Zhou, Yihua
 APPLICANT Kovalic, David K.
 APPLICANT Screen, Steven E
 APPLICANT Tabaska, Jack E
 APPLICANT Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53313) B

; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO: 73120
 ; LENGTH: 452
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE: OTHER INFORMATION: Clone ID: UC-ZMFLB73270E12_FLI.pep
 ; US-10-425-114-71520
 Query Match 1.9%; Score 118; DB 12; Length 452;
 Best Local Similarity 22.7%; Pred. No. 0, 0.052;
 Matches 91; Conservative 36; Mismatches 132; Indels 142; Gaps 22;
 Qy 195 PVQLEMPDYNRLVPDPFNTHRSIGEGFVYPTPYNTGLCHLIDCV-TAPMAVALRTRV 254
 Db 90 PVQRTRPVSTEAVPQ-----HH----ODDIETS-NSGSSKKIEDCI-----126
 Qy 255 TAVARGAAHAFDENHEGAVLPPDITYTYFQSSSGTTARGARRNDNTNSTSKPSGSG- 312
 Db 127 -----ASSEN-----LPPD-----GTTNVEVTDANASSONLSPGYS 160
 Qy 313 -----GPERRLA-----SIMAADT-----ALHAEVIFT 336
 Db 161 STKVYEDIAELSGFNKDKAGSNVFGTSSVEAVQSRDLYHFISLFLHDFVNL 220
 Qy 337 GIYEETPTD1KEWMFPIGMETPLRNALGSTMAYPSNSALYTEVEDSG 396
 Db 221 NYFOSS-----ILGBENS---NKDGSOQ---EGSGENDY-----DHK 252
 Qy 397 MTEAKDGGPPSFNRYQ--FASP--HLAA-----NPQTDRGHTLSSCST--G 439
 Db 253 QAEXAKMGAKGSQDFGIDKSIPKPTEPFLTVMLKLWNNKERIDKASDVYQSSTOYNEA 312
 Qy 440 SSNTFSVYDYLALICFGAPLLARLFLYLERCDAGFTGHGDALKYTTGTFDSEIPCSL 499
 Db 313 LENPISIQLRGHTCMKGPKARVY-TPVLEVGS-EGRLNACKVITDAF--IKAGI 367
 Qy 500 C-EKHTRPGCAHTTYHRLRORMPREGQAT---RQPIGYFG 535
 Db 368 VFERDRELKHTATMVNRHRSRNKRNTWTDSDARGIFG 408

RESULT 30
 US-10-084-846A-8
 Sequence 8, Application US/100084846A
 Publication No. US20040060626A1
 GENERAL INFORMATION:
 APPLICANT: WEITNAUER, GABRIELE
 APPLICANT: MOHLWNE, AGNES
 APPLICANT: TREZER, AXEL
 APPLICANT: BECHTHOLD, ANDREAS
 TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 FILE REFERENCE: 1974-005
 CURRENT APPLICATION NUMBER: US/10/084,846A
 PRIOR APPLICATION NUMBER: 2001-08-24
 CURRENT FILING DATE: 2003-02-25
 PRIOR FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: DB 101 09 166 .4
 NUMBER OF SEQ ID NOS: 120
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO: 8
 LENGTH: 19608
 TYPE: PRT
 ORGANISM: Streptomyces viridochromogenes
 FEATURE:
 OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
 OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
 US-10-084-846A-8

Query Match 1.9%; Score 118; DB 15; Length 19608;

Best Local Similarity 19.7%; Pred. No. 44;	Mismatches 443; Indels 404; Gaps 62;	Db 12590 CVDAAWPSAVGCSVVR-- SVRSTMSLAVGSFORMLAGIS-----RERRF----	12631
Matches 240; Conservative 133;	Qy 106 APNTRACNAAREPFGFSSC---QGPVPGDAVETTGAE----ICTRIGLEP-----149	Qy 1033 GFICPVTTGPSSGNRETTLSDOVRGTLIVSGAMVOLAIYATVRAVGARAGHMAFDWLSL 1092	
	Db 11736 APHSPPTRGARPGRHRGRGRGPIPGA---RGAPPHASRSLRSRSDSAPSNTL 11792	Db 12332 -----SSRRRTTIVTESSPCSTSG-----RRTCAVGSRSICAI---CSR 12670	
	Qy 150 --ENTILYLVVTAFLKEAVFMCNVFLHYGLDIVH--INHGD-----VIRIPPLEP 195	Qy 1093 TDEELARDLEELHOIQTLETPTVVEGAEALKILLEKITAAGGETPTNLAFNFSCE 11152	
	Db 11793 ENLENNAKQFRIRSAGKKA-----GGLSPSHGCCRQSHAVQRALVQRLPPV 11842	Db 12671 TSSS-----R 12664	
	Qy 196 VOLMPD-----VNRLVPDPENTHERSIEGFVVV-PPTFYNT 231	Qy 1153 PSHDITSVNLNISGSNSIGS 1172	
	Db 11843 V-LGPARGVGEALLERHTGCVABEAEGAVQRPVAVV-----SLPVGYTLDPPVPGAQ 11895	Db 12285 PANDITSASAPPGSSSVSGA 12704	
	Qy 232 GLCHLHDCTVIAPKAVALVRNNTAVARGAAHLAEDENHE-----GAVLP-PDTITYTYFO 285	RESULT 31	
	Db 11896 GVOOQLRQFQIGLG---RARDVYDLP-----QPAFGDQDAPAHVGHVHPVPPAAATPVO 11949	US-10-231-956A-325 ; Sequence 325, Application US/10231956A	
	Qy 286 SSSGGTTTAGGARRNDVNSTSCKPSGGFERLLAS-IMAADTALHAEVFTNTGYIETP 343	; GENERAL INFORMATION:	
	Db 11950 RDAYAQOPGEORNDL-----LRELJGPVVAAPRAHRO-----11985	; APPLICANT: Llorens, James B.	
	Qy 344 TDIXEWPMFIMGEMLPLPRINA-LGSYTAVAG-----VIGANVFSPNSA 386	; APPLICANT: Xu, Weiduan	
	Db 11986 -----PMGRGV-GEGDAYAARLGRRVGRVGGDERVLVPGARLDAAVLVLGDLHDFGRA 12038	; APPLICANT: Bogenberger, Jakob	
	Qy 387 --LYTVEVDS--GMTEAKDGGFPSPNRFYQ-----FAGPHLAANPQTDRDGHYL 434	; APPLICANT: Holland, Sacha	
	Db 12039 GLQAHJHECJDALRHGTYYERRVGRVGDPRVDFGRVGDHQVAGDHGLGQPGI-ADVAVHE 12097	; APPLICANT: Rigel Pharmaceuticals, Incorporated	
	Qy 435 SQSTGSNTFSVSYDALICFGAPLARLFYLERCDAGAFTCGHGDALKYTG-----489	; TITLE OF INVENTION: Modulators of Angiogenesis	
	Db 12098 GVPAGBDRLLQRQVPGVQLYQHGHPERRIAV-----PDDFAHYLGADPAR 12141	; FILE REFERENCE: 021044-004100US	
	Qy 490 -TFDSEIPCSLCERETRVPQAHTYHRLRMRPREGQATRQPGVFTMNSQYSDCBPLG 548	; CURRENT APPLICATION NUMBER: US/10/231,956A	
	Db 12142 STDDQDVPSPF--RTRAATSHVPSYSLRIRVRPRLRPPWT-RLWSPSPSRCAYDV 12197	; NUMBER OF SEQ ID NOS: 522	
	Qy 549 NYAPYLIRKPGDQTEAAKTMQDYRATERLFLIDB0RLLD---RGAPCSSEGSS 604	; SOFTWARE: FastSEQ for Windows Version 3.0	
	Db 12198 RGAFTSVSPRITESSTRAPSIEAPRSIE-YWISLCATRQLPSMEYKGPRESCCTVSG 12256	; SEQ ID NO: 325	
	Qy 605 VIVDHPTFR-----ILDTR--ARIEQTTOFMKVLYETRDYKIREGSEATHMSA-- 654	; LENGTH: 1479	
	Db 12257 PMTAGPTMRREPEIFAPASTTRPTSSLASSTPSMRV--SRDSSRCRPIRSVTLATS 12313	; TYPE: PRX	
	Qy 655 -----LTEDPYSGAFOPITNLVKTTHLAVQDLALSOCVFGQOEGRNFRNQ-----705	; ORGANISM: Homo sapiens	
	Db 12314 FQYRSITVEPTS--CP-----WSASC---RASVISSFFQDGMP 12349	US-10-231-956A-325	
	Qy 706 -----FQPVLRFFFYDLENGGPFISTRITVTLSEGPVSAPNPTL-GODAPAGRT 753	Query Match Score 1.8%; Best Local Similarity 18.5%; Pred. No. 0.97; Length 1479;	
	Db 12350 ATASCTAELKAYPTAARSL-LGSGWP-STTAVTRPFS---SSATPNLRGSAATRANT 12403	Conservative 204; Mismatches 118; Indels 341; Gaps 47;	
	Qy 754 FDGDLLR---VSVEVTRDIRYKVRVFFSGNCNTNISBEAARLVLGLASAVQRQEKRVDMLH 810	162 FKEBAVMCNVFLHYGGDIVHINHGDVDTRIPLEFVPMFD--VNRVLPDPDNTHRHSIG 219	
	Db 12404 CAAGLSSRKSAKSIMPSTLSPRM-----TKSSSPRSRDTSTASASPR-----12449	130 FKCLASLQEQLYHFHQET--LDPDSFHQLPKLE-RFLPHNRRITHVPGTFN-HLESMK 185	
	Qy 811 GALGFLIKOFGLLFPFRGMPPNSKSNPONFW-----TLLQRNQMPADL--THEBT 861	220 EGFVYPPTPEYNTGLCHLIHDCVYTAPMVALVRVNTAVARGAAHIAFDENHEGAVLPDPI 279	
	Db 12450 GASCWNTS-----RPNNS-ADSPTAWISAVAPTTIPSDIPASLMEESTRTV 12498	186 RLRLDS---NRLHCC---DCBLWLDLKLTYAESNAQAAICEYPRR-----227	
	Qy 862 TIAAVKRTFTEYAAI--NFINLPPCTIGELAQFTMANLILKYCDHSQYINTLTSITGA 919	280 TTYYFQSSSGTTARGARRNDVNSTSKEPSGGFERRLASTMAATTALHAEVIFTNGIY 339	
	Db 12499 LIATGTSCLAEVCVIGRSLSBP-----NMSAFISHTRSA---12536	228 ---IGRSVATITPEELNCERPRITEPQ-----TIPRINAL-----GSYTTARYVAGVIG 377	
	Qy 920 RRPRDPSSVLMWIKDVTSAADIEQAKALLEKTNLPELWTTARTSTHIVRAMNORM 979	265 FTCAEGRNPKPETIMFNLNLMSMKTUSRLNLDGTLMQNTQETDQGIYOCMANKVAG 324	
	Db 12537 ----PSDQV--VSRELQMAAMSACQFTSRMVFQFPRPGRLARPHAVPCHELRSLQ 12589	378 AMVFSPIANSALYLTVEVSOGMTBAKDGPPGSPNRFYQFAGPHALAQNFTDR---DGHVIL 433	
	Qy 980 VV-----LGISISKYHAGLGNRNVFAQWNSGLNGKRVCPLEFDRTRRIACPRG 1032	325 -----EVKQEVILRYFGSP-----ARPTFVIQNTEVLYGEVTVL 361	
	Db 411 ACBATNNDIS-----VATAFTIVQAPQFVTPQDBEVIEQTVDFQ-- 453	434 SSQSTG-----SSNTERFVDYLALICSGFAPLARLFYLERCDAGFTGGGGDA 483	
	Qy 362 ECPATGHPPPRISWTRGDRTPLEPDPRVNITPSGG-----LYIQ--NVVQGDSEY 410	362 ECPATGHPPPRISWTRGDRTPLEPDPRVNITPSGG-----LYIQ--NVVQGDSEY 410	
	Qy 484 LKVYTGTFDSEIFCSLCEKHTRPVCAHTVHLRORMPRFGQATROPIGVFG-TWNSQYS 542	484 LKVYTGTFDSEIFCSLCEKHTRPVCAHTVHLRORMPRFGQATROPIGVFG-TWNSQYS 542	
	Db 543 DCDPGLNQAPYLILRKEDQTEAKATMQDTYRATERLRLFIDLEQERLLDRGA-PCSEG 601	411 ACBATNNDIS-----VATAFTIVQAPQFVTPQDBEVIEQTVDFQ-- 453	
	Db 454 -CBAKGNPBPPVIAWTKGQSOLSV-----DREHLVSSGTRISGVALHDQGQECAVN 506	543 DCDPGLNQAPYLILRKEDQTEAKATMQDTYRATERLRLFIDLEQERLLDRGA-PCSEG 601	

RESULT 32
 US-10-211-462-87
 ; Sequence 87, Application US/10211462
 ; Publication No. US20040033495A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Angiogenesis, Compositions and
 ; Methods of Screening for Angiogenesis Modulators
 ; FILE REFERENCE: 018511-00200US
 ; CURRENT APPLICATION NUMBER: US/10/211,462
 ; CURRENT FILING DATE: 2003-02-13
 ; PRIOR APPLICATION NUMBER: US 09/784,356
 ; PRIOR FILING DATE: 2001-02-14
 ; PRIOR APPLICATION NUMBER: US 09/791,390
 ; PRIOR FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: US 60/310,025
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 60/334,244
 ; PRIOR FILING DATE: 2001-11-29
 ; NUMBER OF SEQ ID NOS: 230
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 87
 ; LENGTH: 1495
 ; TYPE: PRT

ORGANISM: Homo sapiens
 US-10-211-462-87

Query Match 1.8%; Score 114.5; DB 12; Length 1496;
 Best Local Similarity 18.5%; Pred. No. 0.99; Mismatches 441; Indels 341; Gaps 47;
 Matches 204; Conservative 118; Miatches 618; Miatches 441; Indels 341; Gaps 47;

Qy 561 DGVQVTBESGGKFFISPEGFLITINDVGPAADAGRYECV----ARNTIGSSAVSMYLSTAVN 613
 Db 715 VDLFNGG--FIST-----RSITVT--LSEGVP SAPNPTLG-----QDA 748
 Db 614 DVSRRNGDPFPEVATSVIBAATYDRA-INSTRTLFDSPRSPNDLALFRYPRDPYVEQA 673
 Qy 749 PAGRFTDDOLARYSVENTRDIRVK-----NRYVFSGNCTNLSEAAAR 791
 Db 674 RAGEFIFERTLQIJOHQHQLMVDLNGTSYHYNDLSPQVNLIANLSCCT-----AHR 728
 Qy 792 LVGLASAYQRQERXV-----DMLHLGALGFLLRQFGQL-----PRGMPPN--- 832
 Db 729 VNNSCSDMCFHQKYRTHGTCNNLQHPWNGASITAFLKLKVSYENGFNTGRINPHRLYN 788
 Qy 833 SKSPNPNOWFWTLIQRNOMPADKLTHEEITTIAAVK--RFTEE 872
 Db 789 GHALMPMPRLVSLTILGIVETVTPDEQFTHMLQWQF---LDHLDSTTVALSQAFSDG 844
 Qy 873 YAAINPNNLPPTCI-----GELQFYMANLILKCYDHSQYLNTLTSITGA 919
 Db 845 OHCSNVCSNDPPEFSVNMIPPDNSRARSACRNFFVR-----BPGCSGMTSLMNS 896
 Qy 920 RRPPDPSSVWLHWTRKDVTSAADIEQAKALLEKTENLPELNTAFTSITH--LVRAAMNQ 977
 Db 897 VYREQINQL-----TSYIDASNYVGSTEEHARSIRDL-----ASHRGILROIVQR 943
 Qy 978 PMTVLGISSSKYHGAAGNTRVFOAGNNGLNGSKNVPPLFTDRTRRFLIACPR---GG 1033
 Db 944 -----SGKPLIPPAIGSPTE---CMRDENESP 967
 Qy 1034 EICPYTGPSBGSNRETTLSQ---VRGTTIVSGAMVOL-----AIYATVYRAGARAQ 1082
 Db 968 1PCPLAGDIRURANBGLJSMHTIWPREINRIATELLKUNPHDGTIYYETRKVGAIIQ 1027
 Qy 1083 HMAFDDMLSITDDEFLANDLEELH 1106
 Db 1028 HITYQHMLPKILGEVGMRTEGYH 1051
 RESULT 32
 US-10-211-462-87
 ; Sequence 87, Application US/10211462
 ; Publication No. US20040033495A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Angiogenesis, Compositions and
 ; Methods of Screening for Angiogenesis Modulators
 ; FILE REFERENCE: 018511-00200US
 ; CURRENT APPLICATION NUMBER: US/10/211,462
 ; CURRENT FILING DATE: 2003-02-13
 ; PRIOR APPLICATION NUMBER: US 09/784,356
 ; PRIOR FILING DATE: 2001-02-14
 ; PRIOR APPLICATION NUMBER: US 09/791,390
 ; PRIOR FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: US 60/310,025
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 60/334,244
 ; PRIOR FILING DATE: 2001-11-29
 ; NUMBER OF SEQ ID NOS: 230
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 87
 ; LENGTH: 1495
 ; TYPE: PRT

Db	961	-----SGKPPLPFATGGPPT-----CMRDNESP	984	602 L--SSVIVDHPFFRLDLRARIETTQFMKVLFVETRDYKIREGLSEATHSMALTEDP 659
Qy	1034	FICPVTPGSSGNRETTILSDQ---VRGIIIVSGGAMVOL---AIVATYVRAVGARAQ 1082	Qy	624 IIGSQKVTAHLTVQPRVTVPFASTPSDDT-----VEYGANYQLPCSQGEPEPAITNK 577
Db	985	IPOFLAIDBHRANEOLGTSMTMFLWFEHNRATELLKLNPWDGDTIYXTRKTYGAEIQ 1044	Db	660 YSGAFCPCPNTFLYERTHIAVVAODA---LSQOCHCVFYQQQEERNF-RNQFPDVLRRF 714
Qy	1083	RNAFDWLSLTDDEFARLDLBEH 1106	Qy	578 DGQVTTESKEFHISPEGFLITINDVGPADGRYECV-----ARNTIGASYSMVLSTNV 630
Db	1045	HITYQHMLPKLGEVGMRTLGSEYH 1068	Qy	715 VDLFNGG--FIST-----RSITVY---LSEGPIVASPNPTLG-----ODA 748
RESULT 33				
US-10-021-660-125				
Sequence 125, Application US/10021660				
Publication No. US20030152926A1				
GENERAL INFORMATION:				
APPLICANT: Murray, Richard				
APPLICANT: Glynne, Richard				
APPLICANT: Watson, Susan R.				
APPLICANT: Eos Biotechnology, Inc.				
TITLE OF INVENTION: No. US2003012926A1 et al Methods of Diagnosis of Angiogenesis, Compositions and Methods of Screening for Angiogenesis				
TITLE OF INVENTION: Methods of Screening for Angiogenesis				
TITLE OF INVENTION: Modulators				
FILE REFERENCE: 016501-000710US				
CURRENT APPLICATION NUMBER: US/10/021,660				
CURRENT FILING DATE: 2001-12-6				
PRIOR APPLICATION NUMBER: US/09/784,356				
PRIOR FILING DATE: 2001-02-14				
PRIOR APPLICATION NUMBER: US 09 / 637,977				
PRIOR FILING DATE: 2000-08-11				
NUMBER OF SEQ ID NOS: 135				
SOFTWARE: FastSEQ for Windows Version 3.0				
SEQ ID NO: 125				
LENGTH: 1496				
TYPE: PRT				
ORGANISM: Homo sapiens				
US-10-021-660-125				
Query Match 1.8%; Score 114.5; DB 14; Length 1496;				
Best Local Similarity 18.5%; Prod. No. 0.99; Mismatches 441; Indels 341; Gaps 47; Matches 204; Conservative 118; Mismatches 441; Indels 341; Gaps 47;				
Qy	162	FKEAVFMCNVFLHYGGDLDIVHNGDVTRIPLPVQLMPD - VNRLYPPDNTHRSIG 219	Qy	792 LVGLASAYQRQEV-----DMHAGLCLIKQPHGL-----FPRGMPPN---- 832
Db	147	PKGLASLEOLYLHENQIET-LDPDSFQHLPKLE-RLFHLNNRITHLVPGTEN-HLBSMK 202	Db	691 RAGEIFERTQLQIHEQHGLMYDNLGTSYHNDLVSYQNLNLIANLNGCT----ARR 745
Qy	220	EGFTYPTPYNTGHCLHIDCVAPMAVALRVNNTAVARGAAHLDENHGAVLPPDI 279	Qy	749 PAGTIEDGLARSVVEVDIRVK-----NEVVFSCTNLTUSEAABAR 791
Db	203	RLRIDS---NTLHC---DCEIWLADILKTYAEGNAQAALICEPVR-----244	Db	631 PDVSINGDPFVATVEATVDRAINSTRTHLDFSRSPSPNILLALERYPRDPYVQA 690
Qy	280	TYTYFQSSSSGTGTARGARRNDYNTSKESPSGGFERLASSIMAADTAHLHAVIDFTGY 339	Qy	632 L--SSVIVDHPFFRLDLRARIETTQFMKVLFVETRDYKIREGLSEATHSMALTEDP 659
Db	245	---IQGRSATVTPEELNCRPRITSEFQ-----DADUTSGNTVY 281	Db	633 DSEPMALYLTEVEDSGMTEAKDGGGPSFNRFYQZAGPHILANPOTDR---DGHVL 433
Qy	340	BETPDIXKWPFIGMEG---TLRPNAL-----GSTYARVAVGIG 377	Qy	634 -----EVTKTQSTVLLRFQSP-----ARPTEVIOPTNTEVLYGESVTL 378
Db	282	FTCRAEGNPKEIWLNNNIELSNKTDSSLNLDDGTIMQNTQEDGIGYOCMKNVAG 341	Qy	434 SSQSTG-----SSNTBEFSVDYLALLGFAPLLFLYLERCDAGFTGGHGDAA 483
Qy	378	AMVFSNPSNALSILTEVEDSGMTEAKDGGGPSFNRFYQZAGPHILANPOTDR---DGHVL 433	Db	379 ECSAIGHPPRISWRGDRTPLPVDPVNUTPSGG-----LYIQ---NYVQGDSEY 427
Db	342	-----EVTKTQSTVLLRFQSP-----ARPTEVIOPTNTEVLYGESVTL 378	Qy	484 LKYVGTGFDESEIPCSUCXEKTRPVCAHTTTHRQORMPFFQGATRQFGVFG-TMNSOYS 542
Qy	434	-----SSNTBEFSVDYLALLGFAPLLFLYLERCDAGFTGGHGDAA 483	Db	428 ACSATNND-----VHATFIIQALPFTVTPQDRVIEQTVDFQ - 470
Db	379	ECSAIGHPPRISWRGDRTPLPVDPVNUTPSGG-----LYIQ---NYVQGDSEY 427	Qy	543 DCDPLGNYAPYLILRKPGDQTEAKATMDQTYRATERLFLDIDRGA-PCSEG 601
Db	471	-CEAKGNNPPVIAWTKGGSQLSV-----DRRHVLSSSETLRSVGHLDQGOYEQAVN 523	Db	471 -CEAKGNNPPVIAWTKGGSQLSV-----DRRHVLSSSETLRSVGHLDQGOYEQAVN 523

PRIOR APPLICATION NUMBER: US 60/366,869
 PRIORITY FILING DATE: 2002-03-20
 PRIORITY APPLICATION NUMBER: US 60/366,284
 PRIORITY FILING DATE: 2002-03-21
 PRIORITY APPLICATION NUMBER: US 60/368,679
 PRIORITY FILING DATE: 2002-03-28
 PRIORITY APPLICATION NUMBER: US 60/404,809
 PRIORITY FILING DATE: 2002-08-19
 PRIORITY APPLICATION NUMBER: US 60/405,645
 PRIORITY FILING DATE: 2002-08-21
 SEQ ID NO: 28
 LENGTH: 1496
 TYPE: PRY
 ORGANISM: Homo sapien
 US-10-331-49A-28

Query Match Score 114.5; DB 15; Length 1496;
 Best Local Similarity 18.5%; Pred. No. 0; Mismatches 411; Indels 341; Gaps 47;
 Matches 204; Conservative 118; Prior Application Number: US/10276774

Qy 162 FKEAVFMCVFLHVGGLDVIHNGDVIRIPLPVQLEMPD--VNRLYDPFNTFHRSIG 219
 Db 147 FGKLASLQLYLHENQIE--LDPDSFQLPKLE-RFLHNRITHLYPGTEN-HLESMK 202

Qy 220 EGFTYPTPYNTGICLHLIDCVIAPMAVALRVENTVAVARGAHLAEDNHEGAVLPDI 279
 Db 203 RLRLDS---NTLHC---DCEILWLAIDLKTYAEGSNAQAACEPR----
 Qy 280 TYTFQSSSGTTARGARRNDVNSTSKEPSGGCFERRASIMAADTAHAEVNTGIG 339
 Db 245 ---IQGRSYATIPPEBLNCERPRITSEIQQ-----DADYTSCTNVY 281

Qy 340 BETPDKWIKPMFIGMEG-----TLPRINL-----GSYATARVAGVIG 377
 Db 282 FTCAEGNPKPETIWLNNELMSMTDSRNLDDGTUMIQNTOEQDGIIQCMAKNVA 341

Qy 378 AMVFSRPNALYLTVEEDSGMTEAKDGGPSPNSRFYQAGPHLAANPOTDR---DGHVL 433
 Db 342 -----EVXTQETVLRYFGSP-----ARPTTVIQPONTEVVLVGBESTL 378

Qy 434 SSQSTG-----SSNTEPSVDYLALICGCFAPLLAFYLERCDAGAFTGGHGD 483
 Db 379 ECSAIGHPPRISMTRGDTPLPVDPRVNNTPSGG-----LYIQ----NIVQGDGEY 427

Qy 484 LKYVTGTFDSIPICSLCEKHTRVPYCAHTVHRURQRMPPFGQATRQPJGVFG-TMNQSY 542
 Db 428 ACSATNNIDS-----VHACAFITVQALPPTVTPQDRVVIEGTVDFQ-- 470

Qy 543 DCDCPUGNYAAYPLILRKPGDTEBARAKMDTYRATLFRIFIDEQERLDRGA--PCSSG 601
 Db 471 -CEAKGNNPPVIAWTKGGSOLSV-----DRRHLYLSSGTLRISGVALHDQGQECAWN 523

Qy 602 L--SSVYIVDHPTEPRLDILRARTBOTTQFMKVLYTETDYKLREGLSATHSMALADP 659
 Db 524 IIGSOKRVALTHVQPRVTFPASPSDT-----VEGANVQLPCCSSSGEPEPAIWNK 577

Qy 660 YSGAFCPTINFLVLRTHLAVQDLA--LSQLCHCYPQQVEGRNF--RNQFQPVLRFFF 714
 Db 578 DGVQVTESGKPHISPEGFLTINDYGPADASRYECY-----ANTIGASAVNVLSTNV 63.0

Qy 715 VDLFNGS--FIRST-----RSITV-----LSGPVSAFPNPLG-----QDA 748
 Db 631 PDVSRRNGDPFVATSIIVEATVDRAINSTRTHLFDSRSPNDLIALFYPRDPYTVQA 690

Qy 749 PAGRTEFDGDLARVSVEVDIRVK-----NRVYESGRCTNLSBAARAR 791
 Db 691 RAGEIFERTLQIQEHIQHGMVNDINGTSHYNDLVSPQYINLNLANSGT----AHR 745

Qy 792 LVGLASAYQRQEKRV-----DMLGALGFILKQFHLGL-----FPRGMPPN--- 832
 Db 746 VNNSCDMCFHQYRTDHGTCNLQHMMWASLTAFLRLSYYENGFTPRGINPHRLWY 805

Qy 978 PMVNLGISISKYHGAAGNRRVFOAGNWSSLNGKNCVNPCLFEDRTRFTIACPR---GG 1033
 Db 961 -----SGPLPLPATGPPT-----CNRDENESP 984

Qy 1034 FICPYTGPSGSNRETISDQ---VRGLIVSGGAMVQ-----AIYATVVRAGAAQ 1082
 Db 985 IPCFLAGDHANEQOLGLTSMTMWFREINRIATHLICNPHWDGDTTYYETRKVGAETIQ 1044

RESULT 35
 US-10-276-774-1957
 ; Sequence 1957, Application US/10276774
 ; Publication No. US2004004053245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; ATTORNEY OR AGENT: Tang, Y., Tom et al
 ; TITLE OF INVENTION: No. US/10276774
 ; FILE REFERENCE: 21272-030
 ; CURRENT APPLICATION NUMBER: US/10-276-774
 ; PRIOR APPLICATION NUMBER: 09/560,875
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 09/496,914
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 2700
 ; SOFTWARE: Custom
 ; SEQ ID NO: 1957
 ; LENGTH: 1498
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-276-774-1957

Query Match Score 114.5; DB 12; Length 1498;
 Best Local Similarity 18.5%; Pred. No. 0,99; Indels 341; Gaps 47;
 Matches 204; Conservative 118; Mismatches 411; Del/Ins 341; Gaps 47;

Qy 162 FKEAVFMCVFLHVGGLDVIHNGDVIRIPLPVQLEMPD--VNRLYDPFNTFHRSIG 219
 Db 147 FGKLASLQLYLHENQIE--LDPDSFQLPKLE-RFLHNRITHLYPGTEN-HLESMK 202

Qy 220 EGFTYPTPYNTGICLHLIDCVIAPMAVALRVENTVAVARGAHLAEDNHEGAVLPDI 279
 Db 203 RLRLDS---NTLHC---DCEILWLAIDLKTYAEGSNAQAACEPR----
 Qy 280 TYTFQSSSGTTARGARRNDVNSTSKEPSGGCFERRASIMAADTAHAEVNTGIG 339
 Db 245 ---IQGRSYATIPPEBLNCERPRITSEIQQ-----DADYTSCTNVY 281

Qy 340 BETPDKWIKPMFIGMEG-----TLPRINL-----GSYATARVAGVIG 377
 Db 282 FTCAEGNPKPETIWLNNELMSMTDSRNLDDGTUMIQNTOEQDGIIQCMAKNVA 341

Qy 378 AMVFSRPNALYLTVEEDSGMTEAKDGGPSPNSRFYQAGPHLAANPOTDR---DGHVL 433
 Db 342 -----EVXTQETVLRYFGSP-----ARPTTVIQPONTEVVLVGBESTL 378

Qy 434 SSQSTG-----SSNTEPSVDYLALICGCFAPLLAFYLERCDAGAFTGGHGD 483
 Db 379 ECSAIGHPPRISMTRGDTPLPVDPRVNNTPSGG-----LYIQ----NIVQGDGEY 427

Qy 484 LKYVTGTFDSIPICSLCEKHTRVPYCAHTVHRURQRMPPFGQATRQPJGVFG-TMNQSY 542
 Db 428 ACSATNNIDS-----VHACAFITVQALPPTVTPQDRVVIEGTVDFQ-- 470

Qy 543 DCDCPUGNYAAYPLILRKPGDTEBARAKMDTYRATLFRIFIDEQERLDRGA--PCSSG 601
 Db 471 -CEAKGNNPPVIAWTKGGSOLSV-----DRRHLYLSSGTLRISGVALHDQGQECAWN 523

Qy 602 L--SSVYIVDHPTEPRLDILRARTBOTTQFMKVLYTETDYKLREGLSATHSMALADP 659
 Db 524 IIGSOKRVALTHVQPRVTFPASPSDT-----VEGANVQLPCCSSSGEPEPAIWNK 577

Qy 660 YSGAFCPTINFLVLRTHLAVQDLA--LSQLCHCYPQQVEGRNF--RNQFQPVLRFFF 714
 Db 578 DGVQVTESGKPHISPEGFLTINDYGPADASRYECY-----ANTIGASAVNVLSTNV 63.0

Qy 715 VDLFNGS--FIRST-----RSITV-----LSGPVSAFPNPLG-----QDA 748
 Db 631 PDVSRRNGDPFVATSIIVEATVDRAINSTRTHLFDSRSPNDLIALFYPRDPYTVQA 690

Qy 749 PAGRTEFDGDLARVSVEVDIRVK-----NRVYESGRCTNLSBAARAR 791
 Db 691 RAGEIFERTLQIQEHIQHGMVNDINGTSHYNDLVSPQYINLNLANSGT----AHR 745

Qy 792 LVGLASAYQRQEKRV-----DMLGALGFILKQFHLGL-----FPRGMPPN--- 832
 Db 746 VNNSCDMCFHQYRTDHGTCNLQHMMWASLTAFLRLSYYENGFTPRGINPHRLWY 805

Qy 978 PMVNLGISISKYHGAAGNRRVFOAGNWSSLNGKNCVNPCLFEDRTRFTIACPR---GG 1033

Db 379 EGSATGHPPRISWTRGDRTPPLPVDPRVNITPSGG-----LYIQ----NVQGDSGEY 427
 Qy 484 LKVVTCRTRDSEIFPCSLCERKHTRVCANTVIRLQRQMRFOATROPIGVG-TNSQYS 542
 Db 428 ACSATNNIDS-----VHATAPIVQALPQFTVTPQDRVVIEGQTVDQF-- 470
 Qy 543 DCDPLGHNTAPYLILRKPGDQEAAKTMQDTYRATERLFIDLEQERLLDGA -PCSSSEG 601
 Db 471 -CEAKGNDPPVIAWTKGSQLSV-----DRXHLVLISSGTURISGYALHDQYECOAVN 523
 Qy 602 L--SSIVIDHPTERRILDTRARIECTTQFMKVLYETRDYKIREGLSEATHSMALTFDP 659
 Db 524 IIGSQKTVYAHLYQPRVTPFVASIPSDIT-----VEVGANYQLPCSSQGBEPALTWNK 577
 Qy 660 YSGAFCPCPTNFVLYRTHLAVQDIA---LSQCHCIVFYQQYEGRNF -RNQFQVLRRF 714
 Db 578 DGCVQVTESGKFHSPEGFLTINDVGPADAGRYECV-----ARNITGSAVSVMVLSVNV 630
 Qy 715 VDLFNGG -FIST-----RSIVFT--LSEGPPVSAVPNPTLG-----QDA 748
 Db 631 PDYSRNGDBPVATISIVEAIATVDRAINSTRTHFDSPRSRSPNDLLAFRYPRDPYVEQA 690
 Qy 749 PAGRFTFGDPLARYSVEVIRDYRK-----NRVVFSGNCNTLSEARAR 791
 Db 691 RAGIFERTLQLIQBHRVONGMLYDINGTSYHNDLSPQYLNLIANSGCT-----AHRR 745
 Qy 792 LVGLASAYQREQRV-----DMHMGAGFLXKQFHGL-----FPRGMPPN---- 832
 Db 746 VNCCSDMCFHQKZRTHDGTCONLQHMPMGASLTAFERLJKSYYENGNTPRGYNPHLYN 805
 Qy 833 -----SKSPNPQWFNTLQRNQMPADKLTHEETTIAVTK -RFTEE 872
 Db 806 GHALPMPLRVSTLIGTERVTPDQFTMLMQOF----LDHDLSVTVALSQAREFSDG 861
 Qy 873 YAAINFNLPTCT-----GELAQFYMANLILKCDHSQYLINTLTSITGA 919
 Db 862 QHCSSNVCNSNDPPCSVMPPNDARSARSGARCMFVRS-----SPVCGSMTSILMNS 913
 Qy 920 RRPRDPSVSHWIRKDVTSAADIETQAKALLEKTENPLWLTAAFTSPH -LYRAANQR 977
 Db 914 VPREQINQ-----ISYIDAENVYGSTHEARSIRD-----ASHRLLRQIVQR 960
 Qy 978 PMVVLGISISKHYGAAGNNRVRQGNWSGUNG3KRVCPPLFTEDRTRRIACPR---GG 1033
 Db 961 -----SGKPLPPATGPPTE----CNRDNEESP 984
 Qy 1034 FICPVTPGSSGNRETTLSDQ---VRGIIWSSGAMVQ-----AIVATVYRAVGARAQ 1082
 Db 985 IPCFLAGDHANEOLGLTSMHTLAFAEHNRNIATEGRILKUNPHWDGDTIYETRKIVGABIQ 1044
 Qy 1083 HMAFDODWLSLTDDEFLARDJEEHL 1106
 Db 1045 HITQHWLPKILGEVGMRTLGEYH 1068